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(54) Title: RNA INTERFERENCE MEDIATED INHIBITION OF PLATELET DERIVED GROWTH FACTOR (PDGF) AND PLATELET DERIVED GROWTH FACTOR RECEPTOR (PDGFR) GENE EXPRESSION USING SHORT INTERFERING NUCLEIC ACID (siNA)

(57) Abstract: The present invention concerns methods and reagents useful in modulating platelet derived growth factor (PDGF) and platelet derived growth factor receptor (PDGFR) gene expression in a variety of applications, including use in therapeutic, diagnostic, target validation, and genomic discovery applications. Specifically, the invention relates to small nucleic acid molecules, such as short interfering nucleic acid (siNA), short interfering RNA (siRNA), double-stranded RNA (dsRNA), micro-RNA (miRNA), and short hairpin RNA (shRNA) molecules capable of mediating RNA interference (RNAi) against platelet derived growth factor (PDGF) and platelet derived growth factor receptor (PDGFR) gene expression and/or activity. The small nucleic acid molecules are useful in the treatment of oncology conditions, proliferative conditions, inflammatory conditions and any other condition that responds to modulation of PDGF and/or PDGFR expression or activity.



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RNA INTERFERENCE MEDIATED INHIBITION OF PLATELET DERIVED GROWTH FACTOR (PDGF) AND PLATELET DERIVED GROWTH FACTOR RECEPTOR (PDGFR) GENE EXPRESSION USING SHORT INTERFERING NUCLEIC ACID (siNA)

This invention claims the benefit of Beigelman USSN 60/358,580 filed February 20, 2002, of Beigelman USSN 60/363,124 filed March 11, 2002, of Beigelman USSN 60/386,782 filed June 6, 2002, of Beigelman USSN 60/406,784 filed August 29, 2002, of Beigelman USSN 60/408,378 filed September 5, 2002, of Beigelman USSN 60/409,293 filed September 9, 2002, of Beigelman USSN 60/427,467 filed November 19, 2002, and of Beigelman USSN 60/440,129 filed January 15, 2003. These applications are hereby incorporated by reference herein in their entireties, including the drawings.

Field Of The Invention

The present invention concerns compounds, compositions, and methods for the study, diagnosis, and treatment of conditions and diseases that respond to the modulation of platelet derived growth factor (PDGF) and platelet derived growth factor receptor (PDGFr) gene expression and/or activity. The present invention also concerns compounds, compositions, and methods relating to conditions and diseases that respond to the modulation of expression and/or activity of genes involved in PDGF and PDGFr pathways. Specifically, the invention relates to small nucleic acid molecules, such as short interfering nucleic acid (siNA), short interfering RNA (siRNA), double-stranded RNA (dsRNA), micro-RNA (miRNA), and short hairpin RNA (shRNA) molecules capable of mediating RNA interference (RNAi) against PDGF and/or PDGFr genes.

Background Of The Invention

The following is a discussion of relevant art pertaining to RNAi. The discussion is provided only for understanding of the invention that follows. The summary is not an admission that any of the work described below is prior art to the claimed invention.

RNA interference refers to the process of sequence-specific post-transcriptional gene silencing in animals mediated by short interfering RNAs (siRNAs) (Fire *et al.*, 1998, *Nature*, 391, 806). The corresponding process in plants is commonly referred to as post-transcriptional gene silencing or RNA silencing and is also referred to as quelling in

fungi. The process of post-transcriptional gene silencing is thought to be an evolutionarily-conserved cellular defense mechanism used to prevent the expression of foreign genes and is commonly shared by diverse flora and phyla (Fire *et al.*, 1999, *Trends Genet.*, 15, 358). Such protection from foreign gene expression may have evolved in response to the production of double-stranded RNAs (dsRNAs) derived from viral infection or from the random integration of transposon elements into a host genome via a cellular response that specifically destroys homologous single-stranded RNA or viral genomic RNA. The presence of dsRNA in cells triggers the RNAi response through a mechanism that has yet to be fully characterized. This mechanism appears to be different from the interferon response that results from dsRNA-mediated activation of protein kinase PKR and 2',5'-oligoadenylate synthetase resulting in non-specific cleavage of mRNA by ribonuclease L.

The presence of long dsRNAs in cells stimulates the activity of a ribonuclease III enzyme referred to as dicer. Dicer is involved in the processing of the dsRNA into short pieces of dsRNA known as short interfering RNAs (siRNAs) (Berstein *et al.*, 2001, *Nature*, 409, 363). Short interfering RNAs derived from dicer activity are typically about 21 to about 23 nucleotides in length and comprise about 19 base pair duplexes (Elbashir *et al.*, 2001, *Genes Dev.*, 15, 188). Dicer has also been implicated in the excision of 21- and 22-nucleotide small temporal RNAs (stRNAs) from precursor RNA of conserved structure that are implicated in translational control (Hutvagner *et al.*, 2001, *Science*, 293, 834). The RNAi response also features an endonuclease complex, commonly referred to as an RNA-induced silencing complex (RISC), which mediates cleavage of single-stranded RNA having sequence complementary to the antisense strand of the siRNA duplex. Cleavage of the target RNA takes place in the middle of the region complementary to the antisense strand of the siRNA duplex (Elbashir *et al.*, 2001, *Genes Dev.*, 15, 188).

RNAi has been studied in a variety of systems. Fire *et al.*, 1998, *Nature*, 391, 806, were the first to observe RNAi in *C. elegans*. Wianny and Goetz, 1999, *Nature Cell Biol.*, 2, 70, describe RNAi mediated by dsRNA in mouse embryos. Hammond *et al.*, 2000, *Nature*, 404, 293, describe RNAi in *Drosophila* cells transfected with dsRNA. Elbashir *et al.*, 2001, *Nature*, 411, 494, describe RNAi induced by introduction of duplexes of synthetic 21-nucleotide RNAs in cultured mammalian cells including human

embryonic kidney and HeLa cells. Recent work in *Drosophila* embryonic lysates (Elbashir *et al.*, 2001, *EMBO J.*, 20, 6877) has revealed certain requirements for siRNA length, structure, chemical composition, and sequence that are essential to mediate efficient RNAi activity. These studies have shown that 21-nucleotide siRNA duplexes are most active when containing 3'-terminal dinucleotide overhangs. Furthermore, complete substitution of one or both siRNA strands with 2'-deoxy (2'-H) or 2'-O-methyl nucleotides abolishes RNAi activity, whereas substitution of the 3'-terminal siRNA overhang nucleotides with 2'-deoxy nucleotides (2'-H) was shown to be tolerated. Single mismatch sequences in the center of the siRNA duplex were also shown to abolish RNAi activity. In addition, these studies also indicate that the position of the cleavage site in the target RNA is defined by the 5'-end of the siRNA guide sequence rather than the 3'-end of the guide sequence (Elbashir *et al.*, 2001, *EMBO J.*, 20, 6877). Other studies have indicated that a 5'-phosphate on the target-complementary strand of a siRNA duplex is required for siRNA activity and that ATP is utilized to maintain the 5'-phosphate moiety on the siRNA (Nykanen *et al.*, 2001, *Cell*, 107, 309).

Studies have shown that replacing the 3'-terminal nucleotide overhanging segments of a 21-mer siRNA duplex having two -nucleotide 3'-overhangs with deoxyribonucleotides does not have an adverse effect on RNAi activity. Replacing up to four nucleotides on each end of the siRNA with deoxyribonucleotides has been reported to be well tolerated, whereas complete substitution with deoxyribonucleotides results in no RNAi activity (Elbashir *et al.*, 2001, *EMBO J.*, 20, 6877). In addition, Elbashir *et al.*, *supra*, also report that substitution of siRNA with 2'-O-methyl nucleotides completely abolishes RNAi activity. Li *et al.*, International PCT Publication No. WO 00/44914, and Beach *et al.*, International PCT Publication No. WO 01/68836 preliminarily suggest that siRNA may include modifications to either the phosphate-sugar backbone or the nucleoside to include at least one of a nitrogen or sulfur heteroatom, however, neither application postulates to what extent such modifications would be tolerated in siRNA molecules, nor provides any further guidance or examples of such modified siRNA. Kreutzer *et al.*, Canadian Patent Application No. 2,359,180, also describe certain chemical modifications for use in dsRNA constructs in order to counteract activation of double-stranded RNA-dependent protein kinase PKR, specifically 2'-amino or 2'-O-methyl nucleotides, and nucleotides containing a 2'-O or 4'-C methylene bridge.

However, Kreutzer *et al.* similarly fails to provide examples or guidance as to what extent these modifications would be tolerated in siRNA molecules.

Parrish *et al.*, 2000, *Molecular Cell*, 6, 1977-1087, tested certain chemical modifications targeting the unc-22 gene in *C. elegans* using long (>25 nt) siRNA transcripts. The authors describe the introduction of thiophosphate residues into these
5 siRNA transcripts by incorporating thiophosphate nucleotide analogs with T7 and T3 RNA polymerase and observed that RNAs with two phosphorothioate modified bases also had substantial decreases in effectiveness as RNAi. Further, Parrish *et al.* reported that phosphorothioate modification of more than two residues greatly destabilized the
10 RNAs *in vitro* such that interference activities could not be assayed. *Id.* at 1081. The authors also tested certain modifications at the 2'-position of the nucleotide sugar in the long siRNA transcripts and found that substituting deoxynucleotides for ribonucleotides produced a substantial decrease in interference activity, especially in the case of Uridine to Thymidine and/or Cytidine to deoxy-Cytidine substitutions. *Id.* In addition, the
15 authors tested certain base modifications, including substituting, in sense and antisense strands of the siRNA, 4-thiouracil, 5-bromouracil, 5-iodouracil, and 3-(aminoallyl)uracil for uracil, and inosine for guanosine. Whereas 4-thiouracil and 5-bromouracil substitution appeared to be tolerated, Parrish reported that inosine produced a substantial decrease in interference activity when incorporated in either strand. Parrish also reported
20 that incorporation of 5-iodouracil and 3-(aminoallyl)uracil in the antisense strand resulted in a substantial decrease in RNAi activity as well.

The use of longer dsRNA has been described. For example, Beach *et al.*, International PCT Publication No. WO 01/68836, describes specific methods for attenuating gene expression using endogenously-derived dsRNA. Tuschl *et al.*,
25 International PCT Publication No. WO 01/75164, describe a *Drosophila in vitro* RNAi system and the use of specific siRNA molecules for certain functional genomic and certain therapeutic applications; although Tuschl, 2001, *Chem. Biochem.*, 2, 239-245, doubts that RNAi can be used to cure genetic diseases or viral infection due to the danger of activating interferon response. Li *et al.*, International PCT Publication No. WO
30 00/44914, describe the use of specific dsRNAs for attenuating the expression of certain target genes. Zernicka-Goetz *et al.*, International PCT Publication No. WO 01/36646, describe certain methods for inhibiting the expression of particular genes in mammalian

cells using certain dsRNA molecules. Fire *et al.*, International PCT Publication No. WO 99/32619, describe particular methods for introducing certain dsRNA molecules into cells for use in inhibiting gene expression. Plaetinck *et al.*, International PCT Publication No. WO 00/01846, describe certain methods for identifying specific genes responsible for conferring a particular phenotype in a cell using specific dsRNA molecules. Mello *et al.*, International PCT Publication No. WO 01/29058, describe the identification of specific genes involved in dsRNA-mediated RNAi. Deschamps Depaillette *et al.*, International PCT Publication No. WO 99/07409, describe specific compositions consisting of particular dsRNA molecules combined with certain anti-viral agents. Waterhouse *et al.*, International PCT Publication No. 99/53050, describe certain methods for decreasing the phenotypic expression of a nucleic acid in plant cells using certain dsRNAs. Driscoll *et al.*, International PCT Publication No. WO 01/49844, describe specific DNA constructs for use in facilitating gene silencing in targeted organisms.

Others have reported on various RNAi and gene-silencing systems. For example, Parrish *et al.*, 2000, *Molecular Cell*, 6, 1977-1087, describe specific chemically-modified siRNA constructs targeting the unc-22 gene of *C. elegans*. Grossniklaus, International PCT Publication No. WO 01/38551, describes certain methods for regulating polycomb gene expression in plants using certain dsRNAs. Churikov *et al.*, International PCT Publication No. WO 01/42443, describe certain methods for modifying genetic characteristics of an organism using certain dsRNAs. Cogoni *et al.*, International PCT Publication No. WO 01/53475, describe certain methods for isolating a *Neurospora* silencing gene and uses thereof. Reed *et al.*, International PCT Publication No. WO 01/68836, describe certain methods for gene silencing in plants. Honer *et al.*, International PCT Publication No. WO 01/70944, describe certain methods of drug screening using transgenic nematodes as Parkinson's Disease models using certain dsRNAs. Deak *et al.*, International PCT Publication No. WO 01/72774, describe certain *Drosophila*-derived gene products that may be related to RNAi in *Drosophila*. Arndt *et al.*, International PCT Publication No. WO 01/92513 describe certain methods for mediating gene suppression by using factors that enhance RNAi. Tuschl *et al.*, International PCT Publication No. WO 02/44321, describe certain synthetic siRNA constructs. Pachuk *et al.*, International PCT Publication No. WO 00/63364, and Satishchandran *et al.*, International PCT Publication No. WO 01/04313, describe certain

methods and compositions for inhibiting the function of certain polynucleotide sequences using certain dsRNAs. Echeverri *et al.*, International PCT Publication No. WO 02/38805, describe certain *C. elegans* genes identified via RNAi. Kreutzer *et al.*, International PCT Publications Nos. WO 02/055692, WO 02/055693, and EP 1144623 B1 describes certain
5 methods for inhibiting gene expression using RNAi. Graham *et al.*, International PCT Publications Nos. WO 99/49029 and WO 01/70949, and AU 4037501 describe certain vector expressed siRNA molecules. Fire *et al.*, US 6,506,559, describe certain methods for inhibiting gene expression in vitro using certain siRNA constructs that mediate RNAi.

SUMMARY OF THE INVENTION

10 This invention relates to compounds, compositions, and methods useful for modulating the expression of platelet derived growth factor (PDGF) and platelet derived growth factor receptor (PDGFr) gene expression by RNA interference (RNAi) using small nucleic acid molecules, such as short interfering nucleic acid (siNA), short
interfering RNA (siRNA), double-stranded RNA (dsRNA), micro-RNA (miRNA), and
15 short hairpin RNA (shRNA) molecules. In particular, the instant invention features small nucleic acid molecules, such as short interfering nucleic acid (siNA), short interfering RNA (siRNA), double-stranded RNA (dsRNA), micro-RNA (miRNA), and short hairpin RNA (shRNA) molecules and methods used to modulate the expression of PDGF and/or PDGFr genes. A siNA of the invention can be unmodified or chemically-modified. A
20 siNA of the instant invention can be chemically synthesized, expressed from a vector or enzymatically synthesized. The instant invention also features various chemically-modified synthetic short interfering nucleic acid (siNA) molecules capable modulating PDGF and/or PDGFr gene expression or activity in cells by RNA inference (RNAi). The use of chemically-modified siNA is expected to improve various properties of native
25 siNA molecules through increased resistance to nuclease degradation *in vivo* and/or through improved cellular uptake. The siNA molecules of the instant invention provide useful reagents and methods for a variety of therapeutic, diagnostic, target validation, genomic discovery, genetic engineering, and pharmacogenomic applications.

In one embodiment, the invention features one or more siNA molecules and
30 methods that independently or in combination modulate the expression of gene(s) encoding PDGF and/or PDGFr proteins, such as genes encoding sequences comprising

those sequences referred to by GenBank Accession Nos. shown in **Table I**, collectively referred to herein generally as PDGF and/or PDGFr. The description below of the various aspects and embodiments of the invention is provided with reference to exemplary PDGF and PDGFr genes generally referred to herein as PDGF and PDGFr
5 respectively. However, the various aspects and embodiments are also directed to other genes that express other PDGF and PDGFr genes such as mutant PDGF and PDGFr genes and splice variants of PDGF and PDGFr genes. The various aspects and embodiments are also directed to other genes that are involved in the progression, development, or maintenance of cancer and other proliferative diseases such as restenosis. Those
10 additional genes can be analyzed for target sites using the methods described for PDGF and PDGFr herein. Thus, the inhibition and the effects of such inhibition of the other genes can be performed as described herein.

In one embodiment, the invention features a siNA molecule that down-regulates expression of a PDGF gene, for example, wherein the PDGF gene comprises PDGF
15 encoding sequence.

In one embodiment, the invention features a siNA molecule that down-regulates expression of a PDGFr gene, for example, wherein the PDGFr gene comprises PDGFr encoding sequence.

In one embodiment, the invention features a siNA molecule having RNAi activity
20 against PDGF RNA, wherein the siNA molecule comprises a sequence complementary to any RNA having PDGF encoding sequence, such as those sequences having PDGF GenBank Accession Nos. shown in **Table I**. Chemical modifications as shown in **Table IV** or otherwise described herein can be applied to any siNA construct of the invention.

In one embodiment, the invention features a siNA molecule having RNAi activity
25 against PDGFr RNA, wherein the siNA molecule comprises a sequence complementary to any RNA having PDGFr encoding sequence, such as those sequences having PDGFr GenBank Accession Nos. shown in **Table I**. Chemical modifications as shown in **Table IV** or otherwise described herein can be applied to any siNA construct of the invention.

In another embodiment, the invention features a siNA molecule having RNAi
30 activity against a PDGF and/or PDGFr gene, wherein the siNA molecule comprises

nucleotide sequence complementary to nucleotide sequence of a PDGF and/or PDGFr gene, such as those PDGF and/or PDGFr sequences having GenBank Accession Nos. shown in **Table I**. In another embodiment, a siNA molecule of the invention includes nucleotide sequence that can interact with nucleotide sequence of a PDGF and/or PDGFr gene and thereby mediate silencing of PDGF and/or PDGFr gene expression, for example, wherein the siNA mediates regulation of PDGF and/or PDGFr gene expression by cellular processes that modulate the chromatin structure of the PDGF and/or PDGFr gene and prevent transcription of the PDGF and/or PDGFr gene.

In another embodiment, the invention features a siNA molecule comprising nucleotide sequence, for example, nucleotide sequence in the antisense region of the siNA molecule, that is complementary to a nucleotide sequence or portion of sequence of a PDGF and/or PDGFr gene. In another embodiment, the invention features a siNA molecule comprising a region, for example, the antisense region of the siNA construct, complementary to a sequence or portion of sequence comprising a PDGF and/or PDGFr gene sequence.

In one embodiment, the antisense region of PDGFr siNA constructs can comprise a sequence complementary to sequence having any of SEQ ID NOs. 1-311 or 623-626. The antisense region can also comprise sequence having any of SEQ ID NOs. 312-622, 631-634, 639-642, 647-650, 663, 665, 667, 669, 671, or 672. In another embodiment, the sense region of PDGFr constructs can comprise sequence having any of SEQ ID NOs. 1-311, 623-630, 635-638, 643-646, 662, 664, 666, 668, or 670. The sense region can comprise a sequence of SEQ ID NO. 651 and the antisense region can comprise a sequence of SEQ ID NO. 652. The sense region can comprise a sequence of SEQ ID NO. 653 and the antisense region can comprise a sequence of SEQ ID NO. 654. The sense region can comprise a sequence of SEQ ID NO. 655 and the antisense region can comprise a sequence of SEQ ID NO. 656. The sense region can comprise a sequence of SEQ ID NO. 657 and the antisense region can comprise a sequence of SEQ ID NO. 658. The sense region can comprise a sequence of SEQ ID NO. 659 and the antisense region can comprise a sequence of SEQ ID NO. 660. The sense region can comprise a sequence of SEQ ID NO. 657 and the antisense region can comprise a sequence of SEQ ID NO. 661.

In one embodiment, a siNA molecule of the invention comprises any of SEQ ID NOs. 1-672. The sequences shown in SEQ ID NOs: 1-672 are not limiting. A siNA molecule of the invention can comprise any contiguous PDGF and/or PDGFr sequence (e.g., about 19 to about 25, or about 19, 20, 21, 22, 23, 24 or 25 contiguous PDGF and/or PDGFr nucleotides).

In yet another embodiment, the invention features a siNA molecule comprising a sequence, for example the antisense sequence of the siNA construct, complementary to a sequence or portion of sequence comprising sequence represented by GenBank Accession Nos. shown in **Table I**. Chemical modifications in **Tables III and IV** and described herein can be applied to any siRNA construct of the invention.

In one embodiment of the invention a siNA molecule comprises an antisense strand having about 19 to about 29 nucleotides, wherein the antisense strand is complementary to a RNA sequence encoding a PDGF and/or PDGFr protein, and wherein said siNA further comprises a sense strand having about 19 to about 29 (e.g., about 19, 20, 21, 22, 23, 24, 25, 26, 27, 28 or 29) nucleotides, and wherein said sense strand and said antisense strand are distinct nucleotide sequences with at least about 19 complementary nucleotides.

In another embodiment of the invention a siNA molecule of the invention comprises an antisense region having about 19 to about 29 (e.g., about 19, 20, 21, 22, 23, 24, 25, 26, 27, 28 or 29) nucleotides, wherein the antisense region is complementary to a RNA sequence encoding a PDGF and/or PDGFr protein, and wherein said siNA further comprises a sense region having about 19 to about 29 nucleotides, wherein said sense region and said antisense region comprise a linear molecule with at least about 19 complementary nucleotides.

In one embodiment of the invention a siNA molecule comprises an antisense strand comprising a nucleotide sequence that is complementary to a nucleotide sequence or a portion thereof encoding a PDGF and/or PDGFr protein. The siNA further comprises a sense strand, wherein said sense strand comprises a nucleotide sequence of a PDGF and/or PDGFr gene or a portion thereof.

In another embodiment, a siNA molecule comprises an antisense region comprising a nucleotide sequence that is complementary to a nucleotide sequence or a portion thereof encoding a PDGF and/or PDGFr protein. The siNA molecule further comprises a sense region, wherein said sense region comprises a nucleotide sequence of a PDGF and/or PDGFr gene or a portion thereof.

In one embodiment, a siNA molecule of the invention has RNAi activity that modulates expression of RNA encoded by a PDGF and/or PDGFr gene. Because related genes typically share some degree of sequence homology with each other, siNA molecules can be designed to target a class of PDGFr or PDGF genes or alternately specific PDGFr or PDGF genes by selecting sequences that are either shared amongst different PDGFr or PDGF targets or that are alternately unique for a specific PDGFr or PDGF target. Therefore, in one embodiment, the siNA molecule can be designed to target conserved regions of PDGFr or PDGF RNA sequence having homology between several PDGFr or PDGF genes so as to target several PDGFr or PDGF genes (e.g., splice variants, mutant genes etc.) with one siNA molecule. In another embodiment, the siNA molecule can be designed to target a sequence that is unique to a specific PDGFr or PDGF RNA sequence due to the high degree of specificity that the siNA molecule requires to mediate RNAi activity.

In one embodiment, nucleic acid molecules of the invention that act as mediators of the RNA interference gene silencing response are double-stranded nucleic acid molecules. In another embodiment, the siNA molecules of the invention consist of duplexes containing about 19 base pairs between oligonucleotides comprising about 19 to about 25 (e.g., about 19, 20, 21, 22, 23, 24 or 25) nucleotides. In yet another embodiment, siNA molecules of the invention comprise duplexes with overhanging ends of about 1 to about 3 (e.g., about 1, 2, or 3) nucleotides, for example about 21-nucleotide duplexes with about 19 base pairs and 3'-terminal mononucleotide, dinucleotide, or trinucleotide overhangs.

In one embodiment, the invention features one or more chemically-modified siNA constructs having specificity for PDGF and/or PDGFr expressing nucleic acid molecules, such as RNA encoding a PDGF and/or PDGFr protein. Non-limiting examples of such chemical modifications include without limitation phosphorothioate internucleotide

linkages, 2'-deoxyribonucleotides, 2'-O-methyl ribonucleotides, 2'-deoxy-2'-fluoro ribonucleotides, "universal base" nucleotides, "acyclic" nucleotides, 5-C-methyl nucleotides, and terminal glyceryl and/or inverted deoxy abasic residue incorporation. These chemical modifications, when used in various siNA constructs, are shown to
5 preserve RNAi activity in cells while at the same time, dramatically increasing the serum stability of these compounds. Furthermore, contrary to the data published by Parrish *et al.*, *supra*, applicant demonstrates that multiple (greater than one) phosphorothioate substitutions are well-tolerated and confer substantial increases in serum stability for modified siNA constructs.

10 In one embodiment, a siNA molecule of the invention comprises modified nucleotides while maintaining the ability to mediate RNAi. The modified nucleotides can be used to improve *in vitro* or *in vivo* characteristics such as stability, activity, and/or bioavailability. For example, a siNA molecule of the invention can comprise modified nucleotides as a percentage of the total number of nucleotides present in the siNA
15 molecule. As such, a siNA molecule of the invention can generally comprise about 5% to about 100% modified nucleotides (e.g., 5%, 10%, 15%, 20%, 25%, 30%, 35%, 40%, 45%, 50%, 55%, 60%, 65%, 70%, 75%, 80%, 85%, 90%, 95% or 100% modified nucleotides). The actual percentage of modified nucleotides present in a given siNA molecule will depend on the total number of nucleotides present in the siNA.
20 If the siNA molecule is single stranded, the percent modification can be based upon the total number of nucleotides present in the single stranded siNA molecules. Likewise, if the siNA molecule is double stranded, the percent modification can be based upon the total number of nucleotides present in the sense strand, antisense strand, or both the sense and antisense strands.

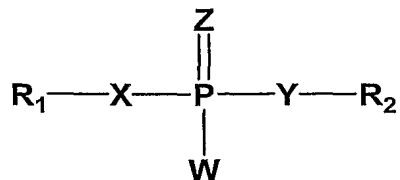
25 In a non-limiting example, the introduction of chemically-modified nucleotides into nucleic acid molecules provides a powerful tool in overcoming potential limitations of *in vivo* stability and bioavailability inherent to native RNA molecules that are delivered exogenously. For example, the use of chemically-modified nucleic acid molecules can enable a lower dose of a particular nucleic acid molecule for a given therapeutic effect
30 since chemically-modified nucleic acid molecules tend to have a longer half-life in serum. Furthermore, certain chemical modifications can improve the bioavailability of nucleic acid molecules by targeting particular cells or tissues and/or improving cellular uptake of

the nucleic acid molecule. Therefore, even if the activity of a chemically-modified nucleic acid molecule is reduced as compared to a native nucleic acid molecule, for example, when compared to an all-RNA nucleic acid molecule, the overall activity of the modified nucleic acid molecule can be greater than that of the native molecule due to improved stability and/or delivery of the molecule. Unlike native unmodified siNA, chemically-modified siNA can also minimize the possibility of activating interferon activity in humans.

The antisense region of a siNA molecule of the invention can comprise a phosphorothioate internucleotide linkage at the 3'-end of said antisense region. The antisense region can comprise about one to about five phosphorothioate internucleotide linkages at the 5'-end of said antisense region. The 3'-terminal nucleotide overhangs of a siNA molecule of the invention can comprise ribonucleotides or deoxyribonucleotides that are chemically-modified at a nucleic acid sugar, base, or backbone. The 3'-terminal nucleotide overhangs can comprise one or more universal base ribonucleotides. The 3'-terminal nucleotide overhangs can comprise one or more acyclic nucleotides.

One embodiment of the invention provides an expression vector comprising a nucleic acid sequence encoding at least one siNA molecule of the invention in a manner that allows expression of the nucleic acid molecule. Another embodiment of the invention provides a mammalian cell comprising such an expression vector. The mammalian cell can be a human cell. The siNA molecule of the expression vector can comprise a sense region and an antisense region. The antisense region can comprise sequence complementary to a RNA or DNA sequence encoding PDGF and/or PDGFr and the sense region can comprise sequence complementary to the antisense region. The siNA molecule can comprise two distinct strands having complementary sense and antisense regions. The siNA molecule can comprise a single strand having complementary sense and antisense regions.

In one embodiment, the invention features a chemically-modified short interfering nucleic acid (siNA) molecule capable of mediating RNA interference (RNAi) against PDGF and/or PDGFr inside a cell or reconstituted *in vitro* system, wherein the chemical modification comprises one or more (*e.g.*, about 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, or more) nucleotides comprising a backbone modified internucleotide linkage having Formula I:

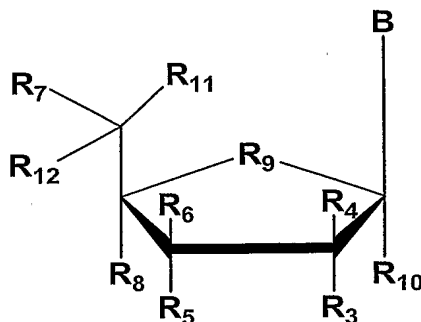


wherein each R1 and R2 is independently any nucleotide, non-nucleotide, or polynucleotide which can be naturally-occurring or chemically-modified, each X and Y is independently O, S, N, alkyl, or substituted alkyl, each Z and W is independently O, S, N, alkyl, substituted alkyl, O-alkyl, S-alkyl, alkaryl, or aralkyl, and wherein W, X, Y, and Z are optionally not all O.

The chemically-modified internucleotide linkages having Formula I, for example, wherein any Z, W, X, and/or Y independently comprises a sulphur atom, can be present in one or both oligonucleotide strands of the siNA duplex, for example, in the sense strand, the antisense strand, or both strands. The siNA molecules of the invention can comprise one or more (*e.g.*, about 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, or more) chemically-modified internucleotide linkages having Formula I at the 3'-end, the 5'-end, or both of the 3' and 5'-ends of the sense strand, the antisense strand, or both strands. For example, an exemplary siNA molecule of the invention can comprise about 1 to about 5 or more (*e.g.*, about 1, 2, 3, 4, 5, or more) chemically-modified internucleotide linkages having Formula I at the 5'-end of the sense strand, the antisense strand, or both strands. In another non-limiting example, an exemplary siNA molecule of the invention can comprise one or more (*e.g.*, about 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, or more) pyrimidine nucleotides with chemically-modified internucleotide linkages having Formula I in the sense strand, the antisense strand, or both strands. In yet another non-limiting example, an exemplary siNA molecule of the invention can comprise one or more (*e.g.*, about 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, or more) purine nucleotides with chemically-modified internucleotide linkages having Formula I in the sense strand, the antisense strand, or both strands. In another embodiment, a siNA molecule of the invention having internucleotide linkage(s) of Formula I also comprises a chemically-modified nucleotide or non-nucleotide having any of Formulae I-VII.

In one embodiment, the invention features a chemically-modified short interfering nucleic acid (siNA) molecule capable of mediating RNA interference (RNAi) against PDGF and/or PDGFr inside a cell or reconstituted *in vitro* system, wherein the chemical

modification comprises one or more (*e.g.*, about 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, or more) nucleotides or non-nucleotides having Formula II:

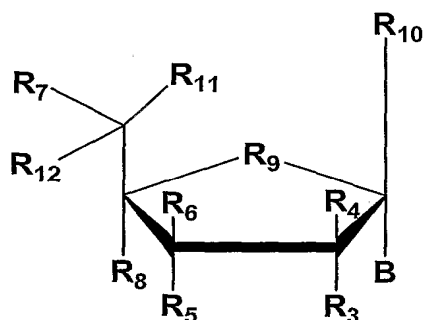


wherein each R3, R4, R5, R6, R7, R8, R10, R11 and R12 is independently H, OH, alkyl, substituted alkyl, alkaryl or aralkyl, F, Cl, Br, CN, CF3, OCF3, OCN, O-alkyl, S-alkyl, N-alkyl, O-alkenyl, S-alkenyl, N-alkenyl, SO-alkyl, alkyl-OSH, alkyl-OH, O-alkyl-OH, O-alkyl-SH, S-alkyl-OH, S-alkyl-SH, alkyl-S-alkyl, alkyl-O-alkyl, ONO2, NO2, N3, NH2, aminoalkyl, aminoacid, aminoacyl, ONH2, O-aminoalkyl, O-aminoacid, O-aminoacyl, heterocycloalkyl, heterocycloalkaryl, aminoalkylamino, polyalkylamino, substituted silyl, or group having Formula I; R9 is O, S, CH2, S=O, CHF, or CF2, and B is a nucleosidic base such as adenine, guanine, uracil, cytosine, thymine, 2-aminoadenosine, 5-methylcytosine, 2,6-diaminopurine, or any other non-naturally occurring base that can be complementary or non-complementary to target RNA or a non-nucleosidic base such as phenyl, naphthyl, 3-nitropyrrole, 5-nitroindole, nebularine, pyridone, pyridinone, or any other non-naturally occurring universal base that can be complementary or non-complementary to target RNA.

The chemically-modified nucleotide or non-nucleotide of Formula II can be present in one or both oligonucleotide strands of the siNA duplex, for example in the sense strand, the antisense strand, or both strands. The siNA molecules of the invention can comprise one or more chemically-modified nucleotide or non-nucleotide of Formula II at the 3'-end, the 5'-end, or both of the 3' and 5'-ends of the sense strand, the antisense strand, or both strands. For example, an exemplary siNA molecule of the invention can comprise about 1 to about 5 or more (*e.g.*, about 1, 2, 3, 4, 5, or more) chemically-modified nucleotides or non-nucleotides of Formula II at the 5'-end of the sense strand, the antisense strand, or both strands. In another non-limiting example, an exemplary siNA molecule of the invention can comprise about 1 to about 5 or more (*e.g.*, about 1, 2, 3, 4,

5, or more) chemically-modified nucleotides or non-nucleotides of Formula II at the 3'-end of the sense strand, the antisense strand, or both strands.

In one embodiment, the invention features a chemically-modified short interfering nucleic acid (siNA) molecule capable of mediating RNA interference (RNAi) against PDGF and/or PDGFr inside a cell or reconstituted *in vitro* system, wherein the chemical modification comprises one or more (*e.g.*, about 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, or more) nucleotides or non-nucleotides having Formula III:



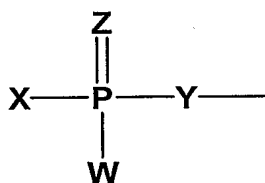
wherein each R3, R4, R5, R6, R7, R8, R10, R11 and R12 is independently H, OH, alkyl, substituted alkyl, alkaryl or aralkyl, F, Cl, Br, CN, CF3, OCF3, OCN, O-alkyl, S-alkyl, N-alkyl, O-alkenyl, S-alkenyl, N-alkenyl, SO-alkyl, alkyl-OSH, alkyl-OH, O-alkyl-OH, O-alkyl-SH, S-alkyl-OH, S-alkyl-SH, alkyl-S-alkyl, alkyl-O-alkyl, ONO2, NO2, N3, NH2, aminoalkyl, aminoacid, aminoacyl, ONH2, O-aminoalkyl, O-aminoacid, O-aminoacyl, heterocycloalkyl, heterocycloalkaryl, aminoalkylamino, polyalkylamino, substituted silyl, or group having Formula I; R9 is O, S, CH2, S=O, CHF, or CF2, and B is a nucleosidic base such as adenine, guanine, uracil, cytosine, thymine, 2-aminoadenosine, 5-methylcytosine, 2,6-diaminopurine, or any other non-naturally occurring base that can be employed to be complementary or non-complementary to target RNA or a non-nucleosidic base such as phenyl, naphthyl, 3-nitropyrrole, 5-nitroindole, nebularine, pyridone, pyridinone, or any other non-naturally occurring universal base that can be complementary or non-complementary to target RNA.

The chemically-modified nucleotide or non-nucleotide of Formula III can be present in one or both oligonucleotide strands of the siNA duplex, for example, in the sense strand, the antisense strand, or both strands. The siNA molecules of the invention can comprise one or more chemically-modified nucleotide or non-nucleotide of Formula

III at the 3'-end, the 5'-end, or both of the 3' and 5'-ends of the sense strand, the antisense strand, or both strands. For example, an exemplary siNA molecule of the invention can comprise about 1 to about 5 or more (*e.g.*, about 1, 2, 3, 4, 5, or more) chemically-modified nucleotide(s) or non-nucleotide(s) of Formula III at the 5'-end of the sense strand, the antisense strand, or both strands. In another non-limiting example, an exemplary siNA molecule of the invention can comprise about 1 to about 5 or more (*e.g.*, about 1, 2, 3, 4, 5, or more) chemically-modified nucleotide or non-nucleotide of Formula III at the 3'-end of the sense strand, the antisense strand, or both strands.

In another embodiment, a siNA molecule of the invention comprises a nucleotide having Formula II or III, wherein the nucleotide having Formula II or III is in an inverted configuration. For example, the nucleotide having Formula II or III is connected to the siNA construct in a 3'-3', 3'-2', 2'-3', or 5'-5' configuration, such as at the 3'-end, the 5'-end, or both of the 3' and 5'-ends of one or both siNA strands.

In one embodiment, the invention features a chemically-modified short interfering nucleic acid (siNA) molecule capable of mediating RNA interference (RNAi) against PDGF and/or PDGFr inside a cell or reconstituted *in vitro* system, wherein the chemical modification comprises a 5'-terminal phosphate group having Formula IV:



wherein each X and Y is independently O, S, N, alkyl, substituted alkyl, or alkylhalo; wherein each Z and W is independently O, S, N, alkyl, substituted alkyl, O-alkyl, S-alkyl, alkaryl, aralkyl, or alkylhalo; and wherein W, X, Y and Z are not all O.

In one embodiment, the invention features a siNA molecule having a 5'-terminal phosphate group having Formula IV on the target-complementary strand, for example, a strand complementary to a target RNA, wherein the siNA molecule comprises an all RNA siNA molecule. In another embodiment, the invention features a siNA molecule having a 5'-terminal phosphate group having Formula IV on the target-complementary strand wherein the siNA molecule also comprises about 1 to about 3 (*e.g.*, about 1, 2, or 3)

nucleotide 3'-terminal nucleotide overhangs having about 1 to about 4 (*e.g.*, about 1, 2, 3, or 4) deoxyribonucleotides on the 3'-end of one or both strands. In another embodiment, a 5'-terminal phosphate group having Formula IV is present on the target-complementary strand of a siNA molecule of the invention, for example a siNA molecule having
5 chemical modifications having any of Formulae I-VII.

In one embodiment, the invention features a chemically-modified short interfering nucleic acid (siNA) molecule capable of mediating RNA interference (RNAi) against PDGF and/or PDGFr inside a cell or reconstituted *in vitro* system, wherein the chemical modification comprises one or more phosphorothioate internucleotide linkages. For
10 example, in a non-limiting example, the invention features a chemically-modified short interfering nucleic acid (siNA) having about 1, 2, 3, 4, 5, 6, 7, 8 or more phosphorothioate internucleotide linkages in one siNA strand. In yet another embodiment, the invention features a chemically-modified short interfering nucleic acid (siNA) individually having about 1, 2, 3, 4, 5, 6, 7, 8 or more phosphorothioate internucleotide linkages in both siNA
15 strands. The phosphorothioate internucleotide linkages can be present in one or both oligonucleotide strands of the siNA duplex, for example in the sense strand, the antisense strand, or both strands. The siNA molecules of the invention can comprise one or more phosphorothioate internucleotide linkages at the 3'-end, the 5'-end, or both of the 3'- and 5'-ends of the sense strand, the antisense strand, or both strands. For example, an
20 exemplary siNA molecule of the invention can comprise about 1 to about 5 or more (*e.g.*, about 1, 2, 3, 4, 5, or more) consecutive phosphorothioate internucleotide linkages at the 5'-end of the sense strand, the antisense strand, or both strands. In another non-limiting example, an exemplary siNA molecule of the invention can comprise one or more (*e.g.*, about 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, or more) pyrimidine phosphorothioate internucleotide
25 linkages in the sense strand, the antisense strand, or both strands. In yet another non-limiting example, an exemplary siNA molecule of the invention can comprise one or more (*e.g.*, about 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, or more) purine phosphorothioate internucleotide linkages in the sense strand, the antisense strand, or both strands.

In one embodiment, the invention features a siNA molecule, wherein the sense
30 strand comprises one or more, for example, about 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, or more phosphorothioate internucleotide linkages, and/or one or more (*e.g.*, about 1, 2, 3, 4, 5, 6, 7, 8, 9, 10 or more) 2'-deoxy, 2'-O-methyl, 2'-deoxy-2'-fluoro, and/or one or more (*e.g.*,

about 1, 2, 3, 4, 5, 6, 7, 8, 9, 10 or more) universal base modified nucleotides, and optionally a terminal cap molecule at the 3'-end, the 5'-end, or both of the 3'- and 5'-ends of the sense strand; and wherein the antisense strand comprises about 1 to about 10 or more, specifically about 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, or more phosphorothioate internucleotide linkages, and/or one or more (*e.g.*, about 1, 2, 3, 4, 5, 6, 7, 8, 9, 10 or more) 2'-deoxy, 2'-O-methyl, 2'-deoxy-2'-fluoro, and/or one or more (*e.g.*, about 1, 2, 3, 4, 5, 6, 7, 8, 9, 10 or more) universal base modified nucleotides, and optionally a terminal cap molecule at the 3'-end, the 5'-end, or both of the 3'- and 5'-ends of the antisense strand. In another embodiment, one or more, for example about 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, or more, pyrimidine nucleotides of the sense and/or antisense siNA strand are chemically-modified with 2'-deoxy, 2'-O-methyl and/or 2'-deoxy-2'-fluoro nucleotides, with or without one or more, for example about 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, or more, phosphorothioate internucleotide linkages and/or a terminal cap molecule at the 3'-end, the 5'-end, or both of the 3'- and 5'-ends, being present in the same or different strand.

In another embodiment, the invention features a siNA molecule, wherein the sense strand comprises about 1 to about 5, specifically about 1, 2, 3, 4, or 5 phosphorothioate internucleotide linkages, and/or one or more (*e.g.*, about 1, 2, 3, 4, 5, or more) 2'-deoxy, 2'-O-methyl, 2'-deoxy-2'-fluoro, and/or one or more (*e.g.*, about 1, 2, 3, 4, 5, or more) universal base modified nucleotides, and optionally a terminal cap molecule at the 3'-end, the 5'-end, or both of the 3'- and 5'-ends of the sense strand; and wherein the antisense strand comprises about 1 to about 5 or more, specifically about 1, 2, 3, 4, 5, or more phosphorothioate internucleotide linkages, and/or one or more (*e.g.*, about 1, 2, 3, 4, 5, 6, 7, 8, 9, 10 or more) 2'-deoxy, 2'-O-methyl, 2'-deoxy-2'-fluoro, and/or one or more (*e.g.*, about 1, 2, 3, 4, 5, 6, 7, 8, 9, 10 or more) universal base modified nucleotides, and optionally a terminal cap molecule at the 3'-end, the 5'-end, or both of the 3'- and 5'-ends of the antisense strand. In another embodiment, one or more, for example about 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, or more, pyrimidine nucleotides of the sense and/or antisense siNA strand are chemically-modified with 2'-deoxy, 2'-O-methyl and/or 2'-deoxy-2'-fluoro nucleotides, with or without about 1 to about 5 or more, for example about 1, 2, 3, 4, 5, or more phosphorothioate internucleotide linkages and/or a terminal cap molecule at the 3'-end, the 5'-end, or both of the 3'- and 5'-ends, being present in the same or different strand.

In one embodiment, the invention features a siNA molecule, wherein the antisense strand comprises one or more, for example, about 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, or more phosphorothioate internucleotide linkages, and/or about one or more (*e.g.*, about 1, 2, 3, 4, 5, 6, 7, 8, 9, 10 or more) 2'-deoxy, 2'-O-methyl, 2'-deoxy-2'-fluoro, and/or one or more (*e.g.*, about 1, 2, 3, 4, 5, 6, 7, 8, 9, 10 or more) universal base modified nucleotides, and optionally a terminal cap molecule at the 3'-end, the 5'-end, or both of the 3'- and 5'-ends of the sense strand; and wherein the antisense strand comprises about 1 to about 10 or more, specifically about 1, 2, 3, 4, 5, 6, 7, 8, 9, 10 or more phosphorothioate internucleotide linkages, and/or one or more (*e.g.*, about 1, 2, 3, 4, 5, 6, 7, 8, 9, 10 or more) 2'-deoxy, 2'-O-methyl, 2'-deoxy-2'-fluoro, and/or one or more (*e.g.*, about 1, 2, 3, 4, 5, 6, 7, 8, 9, 10 or more) universal base modified nucleotides, and optionally a terminal cap molecule at the 3'-end, the 5'-end, or both of the 3'- and 5'-ends of the antisense strand. In another embodiment, one or more, for example about 1, 2, 3, 4, 5, 6, 7, 8, 9, 10 or more pyrimidine nucleotides of the sense and/or antisense siNA strand are chemically-modified with 2'-deoxy, 2'-O-methyl and/or 2'-deoxy-2'-fluoro nucleotides, with or without one or more, for example about 1, 2, 3, 4, 5, 6, 7, 8, 9, 10 or more phosphorothioate internucleotide linkages and/or a terminal cap molecule at the 3'-end, the 5'-end, or both of the 3' and 5'-ends, being present in the same or different strand.

In another embodiment, the invention features a siNA molecule, wherein the antisense strand comprises about 1 to about 5 or more, specifically about 1, 2, 3, 4, 5 or more phosphorothioate internucleotide linkages, and/or one or more (*e.g.*, about 1, 2, 3, 4, 5, 6, 7, 8, 9, 10 or more) 2'-deoxy, 2'-O-methyl, 2'-deoxy-2'-fluoro, and/or one or more (*e.g.*, about 1, 2, 3, 4, 5, 6, 7, 8, 9, 10 or more) universal base modified nucleotides, and optionally a terminal cap molecule at the 3'-end, the 5'-end, or both of the 3'- and 5'-ends of the sense strand; and wherein the antisense strand comprises about 1 to about 5 or more, specifically about 1, 2, 3, 4, 5 or more phosphorothioate internucleotide linkages, and/or one or more (*e.g.*, about 1, 2, 3, 4, 5, 6, 7, 8, 9, 10 or more) 2'-deoxy, 2'-O-methyl, 2'-deoxy-2'-fluoro, and/or one or more (*e.g.*, about 1, 2, 3, 4, 5, 6, 7, 8, 9, 10 or more) universal base modified nucleotides, and optionally a terminal cap molecule at the 3'-end, the 5'-end, or both of the 3'- and 5'-ends of the antisense strand. In another embodiment, one or more, for example about 1, 2, 3, 4, 5, 6, 7, 8, 9, 10 or more pyrimidine nucleotides of the sense and/or antisense siNA strand are chemically-modified with 2'-deoxy, 2'-O-

methyl and/or 2'-deoxy-2'-fluoro nucleotides, with or without about 1 to about 5, for example about 1, 2, 3, 4, 5 or more phosphorothioate internucleotide linkages and/or a terminal cap molecule at the 3'-end, the 5'-end, or both of the 3'- and 5'-ends, being present in the same or different strand.

5 In one embodiment, the invention features a chemically-modified short interfering nucleic acid (siNA) molecule having about 1 to about 5, specifically about 1, 2, 3, 4, 5 or more phosphorothioate internucleotide linkages in each strand of the siNA molecule.

In another embodiment, the invention features a siNA molecule comprising 2'-5' internucleotide linkages. The 2'-5' internucleotide linkage(s) can be at the 3'-end, the 5'-end, or both of the 3'- and 5'-ends of one or both siNA sequence strands. In addition, the
10 2'-5' internucleotide linkage(s) can be present at various other positions within one or both siNA sequence strands, for example, about 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, or more including every internucleotide linkage of a pyrimidine nucleotide in one or both strands of the siNA molecule can comprise a 2'-5' internucleotide linkage, or about 1, 2, 3, 4, 5, 6, 7, 8,
15 9, 10, or more including every internucleotide linkage of a purine nucleotide in one or both strands of the siNA molecule can comprise a 2'-5' internucleotide linkage.

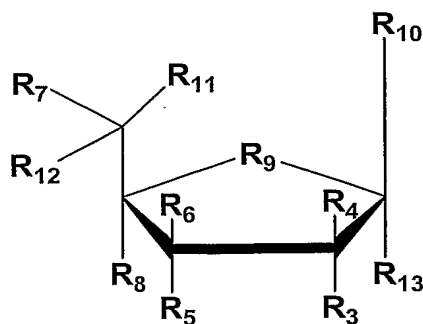
In another embodiment, a chemically-modified siNA molecule of the invention comprises a duplex having two strands, one or both of which can be chemically-modified, wherein each strand is about 18 to about 27 (*e.g.*, about 18, 19, 20, 21, 22, 23, 24, 25, 26,
20 or 27) nucleotides in length, wherein the duplex has about 18 to about 23 (*e.g.*, about 18, 19, 20, 21, 22, or 23) base pairs, and wherein the chemical modification comprises a structure having any of Formulae I-VII. For example, an exemplary chemically-modified siNA molecule of the invention comprises a duplex having two strands, one or both of which can be chemically-modified with a chemical modification having any of Formulae
25 I-VII or any combination thereof, wherein each strand consists of about 21 nucleotides, each having a 2-nucleotide 3'-terminal nucleotide overhang, and wherein the duplex has about 19 base pairs. In another embodiment, a siNA molecule of the invention comprises a single stranded hairpin structure, wherein the siNA is about 36 to about 70 (*e.g.*, about 36, 40, 45, 50, 55, 60, 65, or 70) nucleotides in length having about 18 to about 23 (*e.g.*,
30 about 18, 19, 20, 21, 22, or 23) base pairs, and wherein the siNA can include a chemical modification comprising a structure having any of Formulae I-VII or any combination

thereof. For example, an exemplary chemically-modified siNA molecule of the invention comprises a linear oligonucleotide having about 42 to about 50 (*e.g.*, about 42, 43, 44, 45, 46, 47, 48, 49, or 50) nucleotides that is chemically-modified with a chemical modification having any of Formulae I-VII or any combination thereof, wherein the linear oligonucleotide forms a hairpin structure having about 19 base pairs and a 2-nucleotide 3'-terminal nucleotide overhang. In another embodiment, a linear hairpin siNA molecule of the invention contains a stem loop motif, wherein the loop portion of the siNA molecule is biodegradable. For example, a linear hairpin siNA molecule of the invention is designed such that degradation of the loop portion of the siNA molecule *in vivo* can generate a double-stranded siNA molecule with 3'-terminal overhangs, such as 3'-terminal nucleotide overhangs comprising about 2 nucleotides.

In another embodiment, a siNA molecule of the invention comprises a circular nucleic acid molecule, wherein the siNA is about 38 to about 70 (*e.g.*, about 38, 40, 45, 50, 55, 60, 65, or 70) nucleotides in length having about 18 to about 23 (*e.g.*, about 18, 19, 20, 21, 22, or 23) base pairs, and wherein the siNA can include a chemical modification, which comprises a structure having any of Formulae I-VII or any combination thereof. For example, an exemplary chemically-modified siNA molecule of the invention comprises a circular oligonucleotide having about 42 to about 50 (*e.g.*, about 42, 43, 44, 45, 46, 47, 48, 49, or 50) nucleotides that is chemically-modified with a chemical modification having any of Formulae I-VII or any combination thereof, wherein the circular oligonucleotide forms a dumbbell shaped structure having about 19 base pairs and 2 loops.

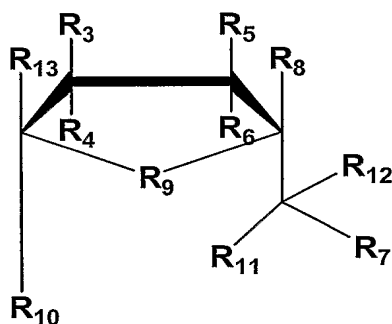
In another embodiment, a circular siNA molecule of the invention contains two loop motifs, wherein one or both loop portions of the siNA molecule is biodegradable. For example, a circular siNA molecule of the invention is designed such that degradation of the loop portions of the siNA molecule *in vivo* can generate a double-stranded siNA molecule with 3'-terminal overhangs, such as 3'-terminal nucleotide overhangs comprising about 2 nucleotides.

In one embodiment, a siNA molecule of the invention comprises at least one (*e.g.*, about 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, or more) abasic moiety, for example a compound having Formula V:



wherein each R3, R4, R5, R6, R7, R8, R10, R11, R12, and R13 is independently H, OH, alkyl, substituted alkyl, alkaryl or aralkyl, F, Cl, Br, CN, CF3, OCF3, OCN, O-alkyl, S-alkyl, N-alkyl, O-alkenyl, S-alkenyl, N-alkenyl, SO-alkyl, alkyl-OSH, alkyl-OH, O-alkyl-OH, O-alkyl-SH, S-alkyl-OH, S-alkyl-SH, alkyl-S-alkyl, alkyl-O-alkyl, ONO2, NO2, N3, NH2, aminoalkyl, aminoacid, aminoacyl, ONH2, O-aminoalkyl, O-aminoacid, O-aminoacyl, heterocycloalkyl, heterocycloalkaryl, aminoalkylamino, polyalkylamino, substituted silyl, or group having Formula I; R9 is O, S, CH2, S=O, CHF, or CF2.

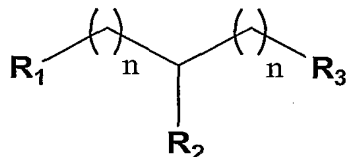
In one embodiment, a siNA molecule of the invention comprises at least one (*e.g.*, about 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, or more) inverted abasic moiety, for example a compound having Formula VI:



wherein each R3, R4, R5, R6, R7, R8, R10, R11, R12, and R13 is independently H, OH, alkyl, substituted alkyl, alkaryl or aralkyl, F, Cl, Br, CN, CF3, OCF3, OCN, O-alkyl, S-alkyl, N-alkyl, O-alkenyl, S-alkenyl, N-alkenyl, SO-alkyl, alkyl-OSH, alkyl-OH, O-alkyl-OH, O-alkyl-SH, S-alkyl-OH, S-alkyl-SH, alkyl-S-alkyl, alkyl-O-alkyl, ONO2, NO2, N3, NH2, aminoalkyl, aminoacid, aminoacyl, ONH2, O-aminoalkyl, O-aminoacid, O-aminoacyl, heterocycloalkyl, heterocycloalkaryl, aminoalkylamino, polyalkylamino, substituted silyl, or group having Formula I; R9 is O, S, CH2, S=O, CHF, or CF2, and

either R2, R3, R8 or R13 serve as points of attachment to the siNA molecule of the invention.

In another embodiment, a siNA molecule of the invention comprises at least one (*e.g.*, about 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, or more) substituted polyalkyl moieties, for example a compound having Formula VII:



wherein each n is independently an integer from 1 to 12, each R1, R2 and R3 is independently H, OH, alkyl, substituted alkyl, alkaryl or aralkyl, F, Cl, Br, CN, CF3, OCF3, OCN, O-alkyl, S-alkyl, N-alkyl, O-alkenyl, S-alkenyl, N-alkenyl, SO-alkyl, alkyl-OSH, alkyl-OH, O-alkyl-OH, O-alkyl-SH, S-alkyl-OH, S-alkyl-SH, alkyl-S-alkyl, alkyl-O-alkyl, ONO2, NO2, N3, NH2, aminoalkyl, aminoacid, aminoacyl, ONH2, O-aminoalkyl, O-aminoacid, O-aminoacyl, heterocycloalkyl, heterocycloalkaryl, aminoalkylamino, polyalkylamino, substituted silyl, or a group having Formula I, and R1, R2 or R3 serves as points of attachment to the siNA molecule of the invention.

In another embodiment, the invention features a compound having Formula VII, wherein R1 and R2 are hydroxyl (OH) groups, $n = 1$, and R3 comprises O and is the point of attachment to the 3'-end, the 5'-end, or both of the 3' and 5'-ends of one or both strands of a double-stranded siNA molecule of the invention or to a single-stranded siNA molecule of the invention. This modification is referred to herein as "glyceryl" (for example modification 6 in **Figure 10**).

In another embodiment, a moiety having any of Formula V, VI or VII of the invention is at the 3'-end, the 5'-end, or both of the 3' and 5'-ends of a siNA molecule of the invention. For example, a moiety having Formula V, VI or VII can be present at the 3'-end, the 5'-end, or both of the 3' and 5'-ends of the antisense strand, the sense strand, or both antisense and sense strands of the siNA molecule. In addition, a moiety having Formula VII can be present at the 3'-end or the 5'-end of a hairpin siNA molecule as described herein.

In another embodiment, a siNA molecule of the invention comprises an abasic residue having Formula V or VI, wherein the abasic residue having Formula VI or VI is connected to the siNA construct in a 3'-3', 3'-2', 2'-3', or 5'-5' configuration, such as at the 3'-end, the 5'-end, or both of the 3' and 5'-ends of one or both siNA strands.

5 In one embodiment, a siNA molecule of the invention comprises one or more (*e.g.*, about 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, or more) locked nucleic acid (LNA) nucleotides, for example at the 5'-end, the 3'-end, both of the 5' and 3'-ends, or any combination thereof, of the siNA molecule.

10 In another embodiment, a siNA molecule of the invention comprises one or more (*e.g.*, about 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, or more) acyclic nucleotides, for example at the 5'-end, the 3'-end, both of the 5' and 3'-ends, or any combination thereof, of the siNA molecule.

15 In one embodiment, the invention features a chemically-modified short interfering nucleic acid (siNA) molecule of the invention, wherein the chemically-modified siNA comprises a sense region, where any (*e.g.*, one or more or all) pyrimidine nucleotides present in the sense region are 2'-deoxy-2'-fluoro pyrimidine nucleotides (*e.g.*, wherein all pyrimidine nucleotides are 2'-deoxy-2'-fluoro pyrimidine nucleotides or alternately a plurality of pyrimidine nucleotides are 2'-deoxy-2'-fluoro pyrimidine nucleotides), and where any (*e.g.*, one or more or all) purine nucleotides present in the sense region are 2'-
20 deoxy purine nucleotides (*e.g.*, wherein all purine nucleotides are 2'-deoxy purine nucleotides or alternately a plurality of purine nucleotides are 2'-deoxy purine nucleotides).

25 In one embodiment, the invention features a chemically-modified short interfering nucleic acid (siNA) molecule of the invention, wherein the chemically-modified siNA comprises a sense region, where any (*e.g.*, one or more or all) pyrimidine nucleotides present in the sense region are 2'-deoxy-2'-fluoro pyrimidine nucleotides (*e.g.*, wherein all pyrimidine nucleotides are 2'-deoxy-2'-fluoro pyrimidine nucleotides or alternately a plurality of pyrimidine nucleotides are 2'-deoxy-2'-fluoro pyrimidine nucleotides), and where any (*e.g.*, one or more or all) purine nucleotides present in the sense region are 2'-
30 deoxy purine nucleotides (*e.g.*, wherein all purine nucleotides are 2'-deoxy purine nucleotides or alternately a plurality of purine nucleotides are 2'-deoxy purine nucleotides).

nucleotides), wherein any nucleotides comprising a 3'-terminal nucleotide overhang that are present in said sense region are 2'-deoxy nucleotides.

In one embodiment, the invention features a chemically-modified short interfering nucleic acid (siNA) molecule of the invention, wherein the chemically-modified siNA comprises an antisense region, where any (*e.g.*, one or more or all) pyrimidine nucleotides present in the antisense region are 2'-deoxy-2'-fluoro pyrimidine nucleotides (*e.g.*, wherein all pyrimidine nucleotides are 2'-deoxy-2'-fluoro pyrimidine nucleotides or alternately a plurality of pyrimidine nucleotides are 2'-deoxy-2'-fluoro pyrimidine nucleotides), and wherein any (*e.g.*, one or more or all) purine nucleotides present in the antisense region are 2'-O-methyl purine nucleotides (*e.g.*, wherein all purine nucleotides are 2'-O-methyl purine nucleotides or alternately a plurality of purine nucleotides are 2'-O-methyl purine nucleotides).

In one embodiment, the invention features a chemically-modified short interfering nucleic acid (siNA) molecule of the invention, wherein the chemically-modified siNA comprises an antisense region, where any (*e.g.*, one or more or all) pyrimidine nucleotides present in the antisense region are 2'-deoxy-2'-fluoro pyrimidine nucleotides (*e.g.*, wherein all pyrimidine nucleotides are 2'-deoxy-2'-fluoro pyrimidine nucleotides or alternately a plurality of pyrimidine nucleotides are 2'-deoxy-2'-fluoro pyrimidine nucleotides), and wherein any (*e.g.*, one or more or all) purine nucleotides present in the antisense region are 2'-O-methyl purine nucleotides (*e.g.*, wherein all purine nucleotides are 2'-O-methyl purine nucleotides or alternately a plurality of purine nucleotides are 2'-O-methyl purine nucleotides), wherein any nucleotides comprising a 3'-terminal nucleotide overhang that are present in said antisense region are 2'-deoxy nucleotides.

In one embodiment, the invention features a chemically-modified short interfering nucleic acid (siNA) molecule of the invention, wherein the chemically-modified siNA comprises an antisense region, where any (*e.g.*, one or more or all) pyrimidine nucleotides present in the antisense region are 2'-deoxy-2'-fluoro pyrimidine nucleotides (*e.g.*, wherein all pyrimidine nucleotides are 2'-deoxy-2'-fluoro pyrimidine nucleotides or alternately a plurality of pyrimidine nucleotides are 2'-deoxy-2'-fluoro pyrimidine nucleotides), and where any (*e.g.*, one or more or all) purine nucleotides present in the antisense region are 2'-deoxy purine nucleotides (*e.g.*, wherein all purine nucleotides are

2'-deoxy purine nucleotides or alternately a plurality of purine nucleotides are 2'-deoxy purine nucleotides).

In one embodiment, the invention features a chemically-modified short interfering nucleic acid (siNA) molecule of the invention capable of mediating RNA interference (RNAi) against PDGF and/or PDGFr inside a cell or reconstituted *in vitro* system, wherein the chemically-modified siNA comprises a sense region, where one or more pyrimidine nucleotides present in the sense region are 2'-deoxy-2'-fluoro pyrimidine nucleotides (e.g., wherein all pyrimidine nucleotides are 2'-deoxy-2'-fluoro pyrimidine nucleotides or alternately a plurality of pyrimidine nucleotides are 2'-deoxy-2'-fluoro pyrimidine nucleotides), and where one or more purine nucleotides present in the sense region are 2'-deoxy purine nucleotides (e.g., wherein all purine nucleotides are 2'-deoxy purine nucleotides or alternately a plurality of purine nucleotides are 2'-deoxy purine nucleotides), and inverted deoxy abasic modifications that are optionally present at the 3'-end, the 5'-end, or both of the 3' and 5'-ends of the sense region, the sense region optionally further comprising a 3'-terminal overhang having about 1 to about 4 (e.g., about 1, 2, 3, or 4) 2'-deoxyribonucleotides; and wherein the chemically-modified short interfering nucleic acid molecule comprises an antisense region, where one or more pyrimidine nucleotides present in the antisense region are 2'-deoxy-2'-fluoro pyrimidine nucleotides (e.g., wherein all pyrimidine nucleotides are 2'-deoxy-2'-fluoro pyrimidine nucleotides or alternately a plurality of pyrimidine nucleotides are 2'-deoxy-2'-fluoro pyrimidine nucleotides), and wherein one or more purine nucleotides present in the antisense region are 2'-O-methyl purine nucleotides (e.g., wherein all purine nucleotides are 2'-O-methyl purine nucleotides or alternately a plurality of purine nucleotides are 2'-O-methyl purine nucleotides), and a terminal cap modification, such as any modification described herein or shown in **Figure 10**, that is optionally present at the 3'-end, the 5'-end, or both of the 3' and 5'-ends of the antisense sequence, the antisense region optionally further comprising a 3'-terminal nucleotide overhang having about 1 to about 4 (e.g., about 1, 2, 3, or 4) 2'-deoxynucleotides, wherein the overhang nucleotides can further comprise one or more (e.g., 1, 2, 3, or 4) phosphorothioate internucleotide linkages. Non-limiting examples of these chemically-modified siNAs are shown in **Figures 4 and 5** and **Tables III and IV** herein.

In one embodiment, the invention features a chemically-modified short interfering nucleic acid (siNA) molecule of the invention capable of mediating RNA interference (RNAi) against PDGF and/or PDGFr inside a cell or reconstituted *in vitro* system, wherein the siNA comprises a sense region, where one or more pyrimidine nucleotides present in the sense region are 2'-deoxy-2'-fluoro pyrimidine nucleotides (e.g., wherein all pyrimidine nucleotides are 2'-deoxy-2'-fluoro pyrimidine nucleotides or alternately a plurality of pyrimidine nucleotides are 2'-deoxy-2'-fluoro pyrimidine nucleotides), and where one or more purine nucleotides present in the sense region are purine ribonucleotides (e.g., wherein all purine nucleotides are purine ribonucleotides or alternately a plurality of purine nucleotides are purine ribonucleotides), and inverted deoxy abasic modifications that are optionally present at the 3'-end, the 5'-end, or both of the 3' and 5'-ends of the sense region, the sense region optionally further comprising a 3'-terminal overhang having about 1 to about 4 (e.g., about 1, 2, 3, or 4) 2'-deoxyribonucleotides; and wherein the siNA comprises an antisense region, where one or more pyrimidine nucleotides present in the antisense region are 2'-deoxy-2'-fluoro pyrimidine nucleotides (e.g., wherein all pyrimidine nucleotides are 2'-deoxy-2'-fluoro pyrimidine nucleotides or alternately a plurality of pyrimidine nucleotides are 2'-deoxy-2'-fluoro pyrimidine nucleotides), and wherein any purine nucleotides present in the antisense region are 2'-O-methyl purine nucleotides (e.g., wherein all purine nucleotides are 2'-O-methyl purine nucleotides or alternately a plurality of purine nucleotides are 2'-O-methyl purine nucleotides), and a terminal cap modification, such as any modification described herein or shown in **Figure 10**, that is optionally present at the 3'-end, the 5'-end, or both of the 3' and 5'-ends of the antisense sequence, the antisense region optionally further comprising a 3'-terminal nucleotide overhang having about 1 to about 4 (e.g., about 1, 2, 3, or 4) 2'-deoxynucleotides, wherein the overhang nucleotides can further comprise one or more (e.g., 1, 2, 3, or 4) phosphorothioate internucleotide linkages. Non-limiting examples of these chemically-modified siNAs are shown in **Figures 4 and 5** and **Tables III and IV** herein.

In one embodiment, the invention features a chemically-modified short interfering nucleic acid (siNA) molecule of the invention capable of mediating RNA interference (RNAi) against PDGF and/or PDGFr inside a cell or reconstituted *in vitro* system, wherein the chemically-modified siNA comprises a sense region, where one or more

pyrimidine nucleotides present in the sense region are 2'-deoxy-2'-fluoro pyrimidine nucleotides (*e.g.*, wherein all pyrimidine nucleotides are 2'-deoxy-2'-fluoro pyrimidine nucleotides or alternately a plurality of pyrimidine nucleotides are 2'-deoxy-2'-fluoro pyrimidine nucleotides), and for example where one or more purine nucleotides present in the sense region are selected from the group consisting of 2'-deoxy nucleotides, locked nucleic acid (LNA) nucleotides, 2'-methoxyethyl nucleotides, 4'-thionucleotides, and 2'-O-methyl nucleotides (*e.g.*, wherein all purine nucleotides are selected from the group consisting of 2'-deoxy nucleotides, locked nucleic acid (LNA) nucleotides, 2'-methoxyethyl nucleotides, 4'-thionucleotides, and 2'-O-methyl nucleotides or alternately a plurality of purine nucleotides are selected from the group consisting of 2'-deoxy nucleotides, locked nucleic acid (LNA) nucleotides, 2'-methoxyethyl nucleotides, 4'-thionucleotides, and 2'-O-methyl nucleotides), and wherein inverted deoxy abasic modifications are optionally present at the 3'-end, the 5'-end, or both of the 3' and 5'-ends of the sense region, the sense region optionally further comprising a 3'-terminal overhang having about 1 to about 4 (*e.g.*, about 1, 2, 3, or 4) 2'-deoxyribonucleotides; and wherein the chemically-modified short interfering nucleic acid molecule comprises an antisense region, where one or more pyrimidine nucleotides present in the antisense region are 2'-deoxy-2'-fluoro pyrimidine nucleotides (*e.g.*, wherein all pyrimidine nucleotides are 2'-deoxy-2'-fluoro pyrimidine nucleotides or alternately a plurality of pyrimidine nucleotides are 2'-deoxy-2'-fluoro pyrimidine nucleotides), and wherein one or more purine nucleotides present in the antisense region are selected from the group consisting of 2'-deoxy nucleotides, locked nucleic acid (LNA) nucleotides, 2'-methoxyethyl nucleotides, 4'-thionucleotides, and 2'-O-methyl nucleotides (*e.g.*, wherein all purine nucleotides are selected from the group consisting of 2'-deoxy nucleotides, locked nucleic acid (LNA) nucleotides, 2'-methoxyethyl nucleotides, 4'-thionucleotides, and 2'-O-methyl nucleotides or alternately a plurality of purine nucleotides are selected from the group consisting of 2'-deoxy nucleotides, locked nucleic acid (LNA) nucleotides, 2'-methoxyethyl nucleotides, 4'-thionucleotides, and 2'-O-methyl nucleotides), and a terminal cap modification, such as any modification described herein or shown in **Figure 10**, that is optionally present at the 3'-end, the 5'-end, or both of the 3' and 5'-ends of the antisense sequence, the antisense region optionally further comprising a 3'-terminal nucleotide overhang having about 1 to about 4 (*e.g.*, about 1, 2, 3, or 4) 2'-

deoxynucleotides, wherein the overhang nucleotides can further comprise one or more (e.g., 1, 2, 3, or 4) phosphorothioate internucleotide linkages.

In another embodiment, any modified nucleotides present in the siNA molecules of the invention, preferably in the antisense strand of the siNA molecules of the invention, but also optionally in the sense and/or both antisense and sense strands, comprise modified nucleotides having properties or characteristics similar to naturally occurring ribonucleotides. For example, the invention features siNA molecules including modified nucleotides having a Northern conformation (e.g., Northern pseudorotation cycle, see for example Saenger, *Principles of Nucleic Acid Structure*, Springer-Verlag ed., 1984). As such, chemically modified nucleotides present in the siNA molecules of the invention, preferably in the antisense strand of the siNA molecules of the invention, but also optionally in the sense and/or both antisense and sense strands, are resistant to nuclease degradation while at the same time maintaining the capacity to mediate RNAi. Non-limiting examples of nucleotides having a northern configuration include locked nucleic acid (LNA) nucleotides (e.g., 2'-O,4'-C-methylene-(D-ribofuranosyl) nucleotides); 2'-methoxyethoxy (MOE) nucleotides; 2'-methyl-thio-ethyl, 2'-deoxy-2'-fluoro nucleotides, 2'-deoxy-2'-chloro nucleotides, 2'-azido nucleotides, and 2'-O-methyl nucleotides.

In one embodiment, the invention features a chemically-modified short interfering nucleic acid molecule (siNA) capable of mediating RNA interference (RNAi) against PDGF and/or PDGFr inside a cell or reconstituted *in vitro* system, wherein the chemical modification comprises a conjugate covalently attached to the chemically-modified siNA molecule. In another embodiment, the conjugate is covalently attached to the chemically-modified siNA molecule via a biodegradable linker. In one embodiment, the conjugate molecule is attached at the 3'-end of either the sense strand, the antisense strand, or both strands of the chemically-modified siNA molecule. In another embodiment, the conjugate molecule is attached at the 5'-end of either the sense strand, the antisense strand, or both strands of the chemically-modified siNA molecule. In yet another embodiment, the conjugate molecule is attached both the 3'-end and 5'-end of either the sense strand, the antisense strand, or both strands of the chemically-modified siNA molecule, or any combination thereof. In one embodiment, a conjugate molecule of the invention comprises a molecule that facilitates delivery of a chemically-modified siNA molecule into a biological system, such as a cell. In another embodiment, the conjugate

molecule attached to the chemically-modified siNA molecule is a poly ethylene glycol, human serum albumin, or a ligand for a cellular receptor that can mediate cellular uptake. Examples of specific conjugate molecules contemplated by the instant invention that can be attached to chemically-modified siNA molecules are described in Vargeese *et al.*, U.S. Serial No. 60/311,865, incorporated by reference herein. The type of conjugates used and the extent of conjugation of siNA molecules of the invention can be evaluated for improved pharmacokinetic profiles, bioavailability, and/or stability of siNA constructs while at the same time maintaining the ability of the siNA to mediate RNAi activity. As such, one skilled in the art can screen siNA constructs that are modified with various conjugates to determine whether the siNA conjugate complex possesses improved properties while maintaining the ability to mediate RNAi, for example in animal models as are generally known in the art.

In one embodiment, the invention features a short interfering nucleic acid (siNA) molecule of the invention, wherein the siNA further comprises a nucleotide, non-nucleotide, or mixed nucleotide/non-nucleotide linker that joins the sense region of the siNA to the antisense region of the siNA. In one embodiment, a nucleotide linker of the invention can be a linker of ≥ 2 nucleotides in length, for example 3, 4, 5, 6, 7, 8, 9, or 10 nucleotides in length. In another embodiment, the nucleotide linker can be a nucleic acid aptamer. By "aptamer" or "nucleic acid aptamer" as used herein is meant a nucleic acid molecule that binds specifically to a target molecule wherein the nucleic acid molecule has sequence that comprises a sequence recognized by the target molecule in its natural setting. Alternately, an aptamer can be a nucleic acid molecule that binds to a target molecule where the target molecule does not naturally bind to a nucleic acid. The target molecule can be any molecule of interest. For example, the aptamer can be used to bind to a ligand-binding domain of a protein, thereby preventing interaction of the naturally occurring ligand with the protein. This is a non-limiting example and those in the art will recognize that other embodiments can be readily generated using techniques generally known in the art. (See, for example, Gold *et al.*, 1995, *Annu. Rev. Biochem.*, 64, 763; Brody and Gold, 2000, *J. Biotechnol.*, 74, 5; Sun, 2000, *Curr. Opin. Mol. Ther.*, 2, 100; Kusser, 2000, *J. Biotechnol.*, 74, 27; Hermann and Patel, 2000, *Science*, 287, 820; and Jayasena, 1999, *Clinical Chemistry*, 45, 1628.)

In yet another embodiment, a non-nucleotide linker of the invention comprises abasic nucleotide, polyether, polyamine, polyamide, peptide, carbohydrate, lipid, polyhydrocarbon, or other polymeric compounds (e.g. polyethylene glycols such as those having between 2 and 100 ethylene glycol units). Specific examples include those described by Seela and Kaiser, *Nucleic Acids Res.* 1990, 18:6353 and *Nucleic Acids Res.* 1987, 15:3113; Cload and Schepartz, *J. Am. Chem. Soc.* 1991, 113:6324; Richardson and Schepartz, *J. Am. Chem. Soc.* 1991, 113:5109; Ma *et al.*, *Nucleic Acids Res.* 1993, 21:2585 and *Biochemistry* 1993, 32:1751; Durand *et al.*, *Nucleic Acids Res.* 1990, 18:6353; McCurdy *et al.*, *Nucleosides & Nucleotides* 1991, 10:287; Jsckke *et al.*, *Tetrahedron Lett.* 1993, 34:301; Ono *et al.*, *Biochemistry* 1991, 30:9914; Arnold *et al.*, International Publication No. WO 89/02439; Usman *et al.*, International Publication No. WO 95/06731; Dudycz *et al.*, International Publication No. WO 95/11910 and Ferentz and Verdine, *J. Am. Chem. Soc.* 1991, 113:4000, all hereby incorporated by reference herein. A "non-nucleotide" further means any group or compound that can be incorporated into a nucleic acid chain in the place of one or more nucleotide units, including either sugar and/or phosphate substitutions, and allows the remaining bases to exhibit their enzymatic activity. The group or compound can be abasic in that it does not contain a commonly recognized nucleotide base, such as adenosine, guanine, cytosine, uracil or thymine, for example at the C1 position of the sugar.

In one embodiment, the invention features a short interfering nucleic acid (siNA) molecule capable of mediating RNA interference (RNAi) inside a cell or reconstituted in vitro system, wherein one or both strands of the siNA molecule that are assembled from two separate oligonucleotides do not comprise any ribonucleotides. All positions within the siNA can include chemically modified nucleotides and/or non-nucleotides such as nucleotides and or non-nucleotides having Formula I, II, III, IV, V, VI, or VII or any combination thereof to the extent that the ability of the siNA molecule to support RNAi activity in a cell is maintained.

In one embodiment, a siNA molecule of the invention is a single stranded siNA molecule that mediates RNAi activity in a cell or reconstituted in vitro system, wherein the siNA molecule comprises a single stranded polynucleotide having complementarity to a target nucleic acid sequence. In another embodiment, the single stranded siNA molecule of the invention comprises a 5'-terminal phosphate group. In another

embodiment, the single stranded siNA molecule of the invention comprises a 5'-terminal phosphate group and a 3'-terminal phosphate group (e.g., a 2',3'-cyclic phosphate). In another embodiment, the single stranded siNA molecule of the invention comprises about 19 to about 29 nucleotides. In yet another embodiment, the single stranded siNA molecule of the invention comprises one or more chemically modified nucleotides or non-nucleotides described herein. For example, all the positions within the siNA molecule can include chemically-modified nucleotides such as nucleotides having any of Formulae I-VII, or any combination thereof to the extent that the ability of the siNA molecule to support RNAi activity in a cell is maintained.

In one embodiment, a siNA molecule of the invention is a single stranded siNA molecule that mediates RNAi activity in a cell or reconstituted in vitro system, wherein the siNA molecule comprises a single stranded polynucleotide having complementarity to a target nucleic acid sequence, and wherein one or more pyrimidine nucleotides present in the siNA are 2'-deoxy-2'-fluoro pyrimidine nucleotides (e.g., wherein all pyrimidine nucleotides are 2'-deoxy-2'-fluoro pyrimidine nucleotides or alternately a plurality of pyrimidine nucleotides are 2'-deoxy-2'-fluoro pyrimidine nucleotides), and wherein any purine nucleotides present in the antisense region are 2'-O-methyl purine nucleotides (e.g., wherein all purine nucleotides are 2'-O-methyl purine nucleotides or alternately a plurality of purine nucleotides are 2'-O-methyl purine nucleotides), and a terminal cap modification, such as any modification described herein or shown in **Figure 10**, that is optionally present at the 3'-end, the 5'-end, or both of the 3' and 5'-ends of the antisense sequence, the siNA optionally further comprising about 1 to about 4 (e.g., about 1, 2, 3, or 4) terminal 2'-deoxynucleotides at the 3'-end of the siNA molecule, wherein the terminal nucleotides can further comprise one or more (e.g., 1, 2, 3, or 4) phosphorothioate internucleotide linkages, and wherein the siNA optionally further comprises a terminal phosphate group, such as a 5'-terminal phosphate group.

In one embodiment, a siNA molecule of the invention is a single stranded siNA molecule that mediates RNAi activity in a cell or reconstituted in vitro system, wherein the siNA molecule comprises a single stranded polynucleotide having complementarity to a target nucleic acid sequence, and wherein one or more pyrimidine nucleotides present in the siNA are 2'-deoxy-2'-fluoro pyrimidine nucleotides (e.g., wherein all pyrimidine nucleotides are 2'-deoxy-2'-fluoro pyrimidine nucleotides or alternately a plurality of

pyrimidine nucleotides are 2'-deoxy-2'-fluoro pyrimidine nucleotides), and wherein any purine nucleotides present in the antisense region are 2'-deoxy purine nucleotides (e.g., wherein all purine nucleotides are 2'-deoxy purine nucleotides or alternately a plurality of purine nucleotides are 2'-deoxy purine nucleotides), and a terminal cap modification, such as any modification described herein or shown in **Figure 10**, that is optionally present at the 3'-end, the 5'-end, or both of the 3' and 5'-ends of the antisense sequence, the siNA optionally further comprising about 1 to about 4 (e.g., about 1, 2, 3, or 4) terminal 2'-deoxynucleotides at the 3'-end of the siNA molecule, wherein the terminal nucleotides can further comprise one or more (e.g., 1, 2, 3, or 4) phosphorothioate internucleotide linkages, and wherein the siNA optionally further comprises a terminal phosphate group, such as a 5'-terminal phosphate group.

In one embodiment, a siNA molecule of the invention is a single stranded siNA molecule that mediates RNAi activity in a cell or reconstituted in vitro system, wherein the siNA molecule comprises a single stranded polynucleotide having complementarity to a target nucleic acid sequence, and wherein one or more pyrimidine nucleotides present in the siNA are 2'-deoxy-2'-fluoro pyrimidine nucleotides (e.g., wherein all pyrimidine nucleotides are 2'-deoxy-2'-fluoro pyrimidine nucleotides or alternately a plurality of pyrimidine nucleotides are 2'-deoxy-2'-fluoro pyrimidine nucleotides), and wherein any purine nucleotides present in the antisense region are locked nucleic acid (LNA) nucleotides (e.g., wherein all purine nucleotides are LNA nucleotides or alternately a plurality of purine nucleotides are LNA nucleotides), and a terminal cap modification, such as any modification described herein or shown in **Figure 10**, that is optionally present at the 3'-end, the 5'-end, or both of the 3' and 5'-ends of the antisense sequence, the siNA optionally further comprising about 1 to about 4 (e.g., about 1, 2, 3, or 4) terminal 2'-deoxynucleotides at the 3'-end of the siNA molecule, wherein the terminal nucleotides can further comprise one or more (e.g., 1, 2, 3, or 4) phosphorothioate internucleotide linkages, and wherein the siNA optionally further comprises a terminal phosphate group, such as a 5'-terminal phosphate group.

In one embodiment, a siNA molecule of the invention is a single stranded siNA molecule that mediates RNAi activity in a cell or reconstituted in vitro system, wherein the siNA molecule comprises a single stranded polynucleotide having complementarity to a target nucleic acid sequence, and wherein one or more pyrimidine nucleotides present in

the siNA are 2'-deoxy-2'-fluoro pyrimidine nucleotides (e.g., wherein all pyrimidine nucleotides are 2'-deoxy-2'-fluoro pyrimidine nucleotides or alternately a plurality of pyrimidine nucleotides are 2'-deoxy-2'-fluoro pyrimidine nucleotides), and wherein any purine nucleotides present in the antisense region are 2'-methoxyethyl purine nucleotides (e.g., wherein all purine nucleotides are 2'-methoxyethyl purine nucleotides or alternately a plurality of purine nucleotides are 2'-methoxyethyl purine nucleotides), and a terminal cap modification, such as any modification described herein or shown in **Figure 10**, that is optionally present at the 3'-end, the 5'-end, or both of the 3' and 5'-ends of the antisense sequence, the siNA optionally further comprising about 1 to about 4 (e.g., about 1, 2, 3, or 4) terminal 2'-deoxynucleotides at the 3'-end of the siNA molecule, wherein the terminal nucleotides can further comprise one or more (e.g., 1, 2, 3, or 4) phosphorothioate internucleotide linkages, and wherein the siNA optionally further comprises a terminal phosphate group, such as a 5'-terminal phosphate group.

In another embodiment, any modified nucleotides present in the single stranded siNA molecules of the invention comprise modified nucleotides having properties or characteristics similar to naturally occurring ribonucleotides. For example, the invention features siNA molecules including modified nucleotides having a Northern conformation (e.g., Northern pseudorotation cycle, see for example Saenger, *Principles of Nucleic Acid Structure*, Springer-Verlag ed., 1984). As such, chemically modified nucleotides present in the single stranded siNA molecules of the invention are preferably resistant to nuclease degradation while at the same time maintaining the capacity to mediate RNAi.

In one embodiment, the invention features a method for modulating the expression of a PDGF and/or PDGFr gene within a cell comprising: (a) synthesizing a siNA molecule of the invention, which can be chemically-modified, wherein one of the siNA strands includes a sequence complementary to RNA of the PDGF and/or PDGFr gene; and (b) introducing the siNA molecule into a cell under conditions suitable to modulate the expression of the PDGF and/or PDGFr gene in the cell.

In one embodiment, the invention features a method for modulating the expression of a PDGF and/or PDGFr gene within a cell comprising: (a) synthesizing a siNA molecule of the invention, which can be chemically-modified, wherein one of the siNA strands includes a sequence complementary to RNA of the PDGF and/or PDGFr gene and

wherein the sense strand sequence of the siNA is identical to the sequence of the target RNA; and (b) introducing the siNA molecule into a cell under conditions suitable to modulate the expression of the PDGF and/or PDGFr gene in the cell.

5 In another embodiment, the invention features a method for modulating the expression of more than one PDGF and/or PDGFr gene within a cell comprising: (a) synthesizing siNA molecules of the invention, which can be chemically-modified, wherein one of the siNA strands includes a sequence complementary to RNA of the PDGF and/or PDGFr genes; and (b) introducing the siNA molecules into a cell under conditions suitable to modulate the expression of the PDGF and/or PDGFr genes in the
10 cell.

In another embodiment, the invention features a method for modulating the expression of more than one PDGF and/or PDGFr gene within a cell comprising: (a) synthesizing a siNA molecule of the invention, which can be chemically-modified, wherein one of the siNA strands includes a sequence complementary to RNA of the
15 PDGF and/or PDGFr gene and wherein the sense strand sequence of the siNA is identical to the sequence of the target RNA; and (b) introducing the siNA molecules into a cell under conditions suitable to modulate the expression of the PDGF and/or PDGFr genes in the cell.

In one embodiment, the invention features a method of modulating the expression
20 of a PDGF and/or PDGFr gene in a tissue explant, comprising: (a) synthesizing a siNA molecule of the invention, which can be chemically-modified, wherein one of the siNA strands includes a sequence complementary to RNA of the PDGF and/or PDGFr gene; and (b) introducing the siNA molecule into a cell of the tissue explant derived from a particular organism under conditions suitable to modulate the expression of the PDGF
25 and/or PDGFr gene in the tissue explant. In another embodiment, the method further comprises introducing the tissue explant back into the organism the tissue was derived from or into another organism under conditions suitable to modulate the expression of the PDGF and/or PDGFr gene in that organism.

In one embodiment, the invention features a method of modulating the expression
30 of a PDGF and/or PDGFr gene in a tissue explant comprising: (a) synthesizing a siNA molecule of the invention, which can be chemically-modified, wherein one of the siNA

strands includes a sequence complementary to RNA of the PDGF and/or PDGFr gene and wherein the sense strand sequence of the siNA is identical to the sequence of the target RNA; and (b) introducing the siNA molecule into a cell of the tissue explant derived from a particular organism under conditions suitable to modulate the expression of the PDGF and/or PDGFr gene in the tissue explant. In another embodiment, the method further comprises introducing the tissue explant back into the organism the tissue was derived from or into another organism under conditions suitable to modulate the expression of the PDGF and/or PDGFr gene in that organism.

In another embodiment, the invention features a method of modulating the expression of more than one PDGF and/or PDGFr gene in a tissue explant comprising: (a) synthesizing siNA molecules of the invention, which can be chemically-modified, wherein one of the siNA strands includes a sequence complementary to RNA of the PDGF and/or PDGFr genes; and (b) introducing the siNA molecules into a cell of the tissue explant derived from a particular organism under conditions suitable to modulate the expression of the PDGF and/or PDGFr genes in the tissue explant. In another embodiment, the method further comprises introducing the tissue explant back into the organism the tissue was derived from or into another organism under conditions suitable to modulate the expression of the PDGF and/or PDGFr genes in that organism.

In one embodiment, the invention features a method of modulating the expression of a PDGF and/or PDGFr gene in an organism comprising: (a) synthesizing a siNA molecule of the invention, which can be chemically-modified, wherein one of the siNA strands includes a sequence complementary to RNA of the PDGF and/or PDGFr gene; and (b) introducing the siNA molecule into the organism under conditions suitable to modulate the expression of the PDGF and/or PDGFr gene in the organism.

In another embodiment, the invention features a method of modulating the expression of more than one PDGF and/or PDGFr gene in an organism comprising: (a) synthesizing siNA molecules of the invention, which can be chemically-modified, wherein one of the siNA strands includes a sequence complementary to RNA of the PDGF and/or PDGFr genes; and (b) introducing the siNA molecules into the organism under conditions suitable to modulate the expression of the PDGF and/or PDGFr genes in the organism.

In one embodiment, the invention features a method for modulating the expression of a PDGF and/or PDGFr gene within a cell, comprising: (a) synthesizing a siNA molecule of the invention, which can be chemically-modified, wherein the siNA comprises a single stranded sequence having complementarity to RNA of the PDGF and/or PDGFr gene; and (b) introducing the siNA molecule into a cell under conditions suitable to modulate the expression of the PDGF and/or PDGFr gene in the cell.

In another embodiment, the invention features a method for modulating the expression of more than one PDGF and/or PDGFr gene within a cell comprising: (a) synthesizing siNA molecules of the invention, which can be chemically-modified, wherein the siNA comprises a single stranded sequence having complementarity to RNA of the PDGF and/or PDGFr gene; and (b) contacting the siNA molecule with a cell in vitro or in vivo under conditions suitable to modulate the expression of the PDGF and/or PDGFr genes in the cell.

In one embodiment, the invention features a method of modulating the expression of a PDGF and/or PDGFr gene in a tissue explant comprising: (a) synthesizing a siNA molecule of the invention, which can be chemically-modified, wherein the siNA comprises a single stranded sequence having complementarity to RNA of the PDGF and/or PDGFr gene; and (b) contacting the siNA molecule with a cell of the tissue explant derived from a particular organism under conditions suitable to modulate the expression of the PDGF and/or PDGFr gene in the tissue explant. In another embodiment, the method further comprises introducing the tissue explant back into the organism the tissue was derived from or into another organism under conditions suitable to modulate the expression of the PDGF and/or PDGFr gene in that organism.

In another embodiment, the invention features a method of modulating the expression of more than one PDGF and/or PDGFr gene in a tissue explant comprising: (a) synthesizing siNA molecules of the invention, which can be chemically-modified, wherein the siNA comprises a single stranded sequence having complementarity to RNA of the PDGF and/or PDGFr gene; and (b) introducing the siNA molecules into a cell of the tissue explant derived from a particular organism under conditions suitable to modulate the expression of the PDGF and/or PDGFr genes in the tissue explant. In another embodiment, the method further comprises introducing the tissue explant back

into the organism the tissue was derived from or into another organism under conditions suitable to modulate the expression of the PDGF and/or PDGFr genes in that organism.

In one embodiment, the invention features a method of modulating the expression of a PDGF and/or PDGFr gene in an organism comprising: (a) synthesizing a siNA molecule of the invention, which can be chemically-modified, wherein the siNA comprises a single stranded sequence having complementarity to RNA of the PDGF and/or PDGFr gene; and (b) introducing the siNA molecule into the organism under conditions suitable to modulate the expression of the PDGF and/or PDGFr gene in the organism.

In another embodiment, the invention features a method of modulating the expression of more than one PDGF and/or PDGFr gene in an organism comprising: (a) synthesizing siNA molecules of the invention, which can be chemically-modified, wherein the siNA comprises a single stranded sequence having complementarity to RNA of the PDGF and/or PDGFr gene; and (b) introducing the siNA molecules into the organism under conditions suitable to modulate the expression of the PDGF and/or PDGFr genes in the organism.

In one embodiment, the invention features a method of modulating the expression of a PDGF and/or PDGFr gene in an organism comprising contacting the organism with a siNA molecule of the invention under conditions suitable to modulate the expression of the PDGF and/or PDGFr gene in the organism.

In another embodiment, the invention features a method of modulating the expression of more than one PDGF and/or PDGFr gene in an organism comprising contacting the organism with one or more siNA molecules of the invention under conditions suitable to modulate the expression of the PDGF and/or PDGFr genes in the organism.

The siNA molecules of the invention can be designed to inhibit target (PDGF and/or PDGFr) gene expression through RNAi targeting of a variety of RNA molecules. In one embodiment, the siNA molecules of the invention are used to target various RNAs corresponding to a target gene. Non-limiting examples of such RNAs include messenger RNA (mRNA), alternate RNA splice variants of target gene(s), post-transcriptionally

modified RNA of target gene(s), pre-mRNA of target gene(s), and/or RNA templates. If alternate splicing produces a family of transcripts that are distinguished by usage of appropriate exons, the instant invention can be used to inhibit gene expression through the appropriate exons to specifically inhibit or to distinguish among the functions of gene family members. For example, a protein that contains an alternatively spliced transmembrane domain can be expressed in both membrane bound and secreted forms. Use of the invention to target the exon containing the transmembrane domain can be used to determine the functional consequences of pharmaceutical targeting of membrane bound as opposed to the secreted form of the protein. Non-limiting examples of applications of the invention relating to targeting these RNA molecules include therapeutic pharmaceutical applications, pharmaceutical discovery applications, molecular diagnostic and gene function applications, and gene mapping, for example using single nucleotide polymorphism mapping with siNA molecules of the invention. Such applications can be implemented using known gene sequences or from partial sequences available from an expressed sequence tag (EST).

In another embodiment, the siNA molecules of the invention are used to target conserved sequences corresponding to a gene family or gene families such as protein tyrosine phosphatase genes. As such, siNA molecules targeting multiple protein tyrosine phosphatase targets can provide increased therapeutic effect. In addition, siNA can be used to characterize pathways of gene function in a variety of applications. For example, the present invention can be used to inhibit the activity of target gene(s) in a pathway to determine the function of uncharacterized gene(s) in gene function analysis, mRNA function analysis, or translational analysis. The invention can be used to determine potential target gene pathways involved in various diseases and conditions toward pharmaceutical development. The invention can be used to understand pathways of gene expression involved in, for example, the progression and/or maintenance of cancer or other proliferative diseases and disorders.

In one embodiment, siNA molecule(s) and/or methods of the invention are used to inhibit the expression of gene(s) that encode RNA referred to by Genbank Accession, for example PDGF and/or PDGFr genes encoding RNA sequence(s) referred to herein by Genbank Accession number, for example Genbank Accession Nos. shown in **Table I**.

In one embodiment, the invention features a method comprising: (a) generating a library of siNA constructs having a predetermined complexity; and (b) assaying the siNA constructs of (a) above, under conditions suitable to determine RNAi target sites within the target RNA sequence. In another embodiment, the siNA molecules of (a) have
5 strands of a fixed length, for example, about 23 nucleotides in length. In yet another embodiment, the siNA molecules of (a) are of differing length, for example having strands of about 19 to about 25 (e.g., about 19, 20, 21, 22, 23, 24, or 25) nucleotides in length. In one embodiment, the assay can comprise a reconstituted *in vitro* siNA assay as described herein. In another embodiment, the assay can comprise a cell culture system in
10 which target RNA is expressed. In another embodiment, fragments of target RNA are analyzed for detectable levels of cleavage, for example by gel electrophoresis, northern blot analysis, or RNase protection assays, to determine the most suitable target site(s) within the target RNA sequence. The target RNA sequence can be obtained as is known in the art, for example, by cloning and/or transcription for *in vitro* systems, and by
15 cellular expression in *in vivo* systems.

In one embodiment, the invention features a method comprising: (a) generating a randomized library of siNA constructs having a predetermined complexity, such as of 4^N , where N represents the number of base paired nucleotides in each of the siNA construct strands (eg. for a siNA construct having 21 nucleotide sense and antisense strands with 19
20 base pairs, the complexity would be 4^{19}); and (b) assaying the siNA constructs of (a) above, under conditions suitable to determine RNAi target sites within the target PDGF and/or PDGFr RNA sequence. In another embodiment, the siNA molecules of (a) have strands of a fixed length, for example about 23 nucleotides in length. In yet another embodiment, the siNA molecules of (a) are of differing length, for example having
25 strands of about 19 to about 25 (e.g., about 19, 20, 21, 22, 23, 24, or 25) nucleotides in length. In one embodiment, the assay can comprise a reconstituted *in vitro* siNA assay as described in Example 7 herein. In another embodiment, the assay can comprise a cell culture system in which target RNA is expressed. In another embodiment, fragments of PDGF and/or PDGFr RNA are analyzed for detectable levels of cleavage, for example by
30 gel electrophoresis, northern blot analysis, or RNase protection assays, to determine the most suitable target site(s) within the target PDGF and/or PDGFr RNA sequence. The target PDGF and/or PDGFr RNA sequence can be obtained as is known in the art, for

example, by cloning and/or transcription for *in vitro* systems, and by cellular expression in *in vivo* systems.

In another embodiment, the invention features a method comprising: (a) analyzing the sequence of a RNA target encoded by a target gene; (b) synthesizing one or more sets of siNA molecules having sequence complementary to one or more regions of the RNA of (a); and (c) assaying the siNA molecules of (b) under conditions suitable to determine RNAi targets within the target RNA sequence. In another embodiment, the siNA molecules of (b) have strands of a fixed length, for example about 23 nucleotides in length. In another embodiment, the siNA molecules of (b) are of differing length, for example having strands of about 19 to about 25 (*e.g.*, about 19, 20, 21, 22, 23, 24, or 25) nucleotides in length. In one embodiment, the assay can comprise a reconstituted *in vitro* siNA assay as described herein. In another embodiment, the assay can comprise a cell culture system in which target RNA is expressed. Fragments of target RNA are analyzed for detectable levels of cleavage, for example by gel electrophoresis, northern blot analysis, or RNase protection assays, to determine the most suitable target site(s) within the target RNA sequence. The target RNA sequence can be obtained as is known in the art, for example, by cloning and/or transcription for *in vitro* systems, and by expression in *in vivo* systems.

By "target site" is meant a sequence within a target RNA that is "targeted" for cleavage mediated by a siNA construct which contains sequences within its antisense region that are complementary to the target sequence.

By "detectable level of cleavage" is meant cleavage of target RNA (and formation of cleaved product RNAs) to an extent sufficient to discern cleavage products above the background of RNAs produced by random degradation of the target RNA. Production of cleavage products from 1-5% of the target RNA is sufficient to detect above the background for most methods of detection.

In one embodiment, the invention features a composition comprising a siNA molecule of the invention, which can be chemically-modified, in a pharmaceutically acceptable carrier or diluent. In another embodiment, the invention features a pharmaceutical composition comprising siNA molecules of the invention, which can be chemically-modified, targeting one or more genes in a pharmaceutically acceptable

carrier or diluent. In another embodiment, the invention features a method for treating or preventing a disease or condition in a subject, comprising administering to the subject a composition of the invention under conditions suitable for the treatment or prevention of the disease or condition in the subject, alone or in conjunction with one or more other
5 therapeutic compounds. In yet another embodiment, the invention features a method for reducing or preventing tissue rejection in a subject comprising administering to the subject a composition of the invention under conditions suitable for the reduction or prevention of tissue rejection in the subject.

In another embodiment, the invention features a method for validating a PDGF
10 and/or PDGFr gene target, comprising: (a) synthesizing a siNA molecule of the invention, which can be chemically-modified, wherein one of the siNA strands includes a sequence complementary to RNA of a PDGF and/or PDGFr target gene; (b) introducing the siNA molecule into a cell, tissue, or organism under conditions suitable for modulating expression of the PDGF and/or PDGFr target gene in the cell, tissue, or
15 organism; and (c) determining the function of the gene by assaying for any phenotypic change in the cell, tissue, or organism.

In another embodiment, the invention features a method for validating a PDGF
and/or PDGFr target comprising: (a) synthesizing a siNA molecule of the invention, which can be chemically-modified, wherein one of the siNA strands includes a sequence
20 complementary to RNA of a PDGF and/or PDGFr target gene; (b) introducing the siNA molecule into a biological system under conditions suitable for modulating expression of the PDGF and/or PDGFr target gene in the biological system; and (c) determining the function of the gene by assaying for any phenotypic change in the biological system.

By "biological system" is meant, material, in a purified or unpurified form, from
25 biological sources, including but not limited to human, animal, plant, insect, bacterial, viral or other sources, wherein the system comprises the components required for RNAi activity. The term "biological system" includes, for example, a cell, tissue, or organism, or extract thereof. The term biological system also includes reconstituted RNAi systems that can be used in an *in vitro* setting.

30 By "phenotypic change" is meant any detectable change to a cell that occurs in response to contact or treatment with a nucleic acid molecule of the invention (e.g.,

siNA). Such detectable changes include, but are not limited to, changes in shape, size, proliferation, motility, protein expression or RNA expression or other physical or chemical changes as can be assayed by methods known in the art. The detectable change can also include expression of reporter genes/molecules such as Green Florescent Protein (GFP) or various tags that are used to identify an expressed protein or any other cellular component that can be assayed.

In one embodiment, the invention features a kit containing a siNA molecule of the invention, which can be chemically-modified, that can be used to modulate the expression of a PDGF and/or PDGFr target gene in a cell, tissue, or organism. In another embodiment, the invention features a kit containing more than one siNA molecule of the invention, which can be chemically-modified, that can be used to modulate the expression of more than one PDGF and/or PDGFr target gene in a cell, tissue, or organism.

In one embodiment, the invention features a cell containing one or more siNA molecules of the invention, which can be chemically-modified. In another embodiment, the cell containing a siNA molecule of the invention is a mammalian cell. In yet another embodiment, the cell containing a siNA molecule of the invention is a human cell.

In one embodiment, the synthesis of a siNA molecule of the invention, which can be chemically-modified, comprises: (a) synthesis of two complementary strands of the siNA molecule; (b) annealing the two complementary strands together under conditions suitable to obtain a double-stranded siNA molecule. In another embodiment, synthesis of the two complementary strands of the siNA molecule is by solid phase oligonucleotide synthesis. In yet another embodiment, synthesis of the two complementary strands of the siNA molecule is by solid phase tandem oligonucleotide synthesis.

In one embodiment, the invention features a method for synthesizing a siNA duplex molecule comprising: (a) synthesizing a first oligonucleotide sequence strand of the siNA molecule, wherein the first oligonucleotide sequence strand comprises a cleavable linker molecule that can be used as a scaffold for the synthesis of the second oligonucleotide sequence strand of the siNA; (b) synthesizing the second oligonucleotide sequence strand of siNA on the scaffold of the first oligonucleotide sequence strand, wherein the second oligonucleotide sequence strand further comprises a chemical moiety than can be used to purify the siNA duplex; (c) cleaving the linker molecule of (a) under conditions suitable

for the two siNA oligonucleotide strands to hybridize and form a stable duplex; and (d) purifying the siNA duplex utilizing the chemical moiety of the second oligonucleotide sequence strand. In another embodiment, cleavage of the linker molecule in (c) above takes place during deprotection of the oligonucleotide, for example under hydrolysis conditions using an alkylamine base such as methylamine. In one embodiment, the method of synthesis comprises solid phase synthesis on a solid support such as controlled pore glass (CPG) or polystyrene, wherein the first sequence of (a) is synthesized on a cleavable linker, such as a succinyl linker, using the solid support as a scaffold. The cleavable linker in (a) used as a scaffold for synthesizing the second strand can comprise similar reactivity as the solid support derivatized linker, such that cleavage of the solid support derivatized linker and the cleavable linker of (a) takes place concomitantly. In another embodiment, the chemical moiety of (b) that can be used to isolate the attached oligonucleotide sequence comprises a trityl group, for example a dimethoxytrityl group, which can be employed in a trityl-on synthesis strategy as described herein. In yet another embodiment, the chemical moiety, such as a dimethoxytrityl group, is removed during purification, for example, using acidic conditions.

In a further embodiment, the method for siNA synthesis is a solution phase synthesis or hybrid phase synthesis wherein both strands of the siNA duplex are synthesized in tandem using a cleavable linker attached to the first sequence which acts as a scaffold for synthesis of the second sequence. Cleavage of the linker under conditions suitable for hybridization of the separate siNA sequence strands results in formation of the double-stranded siNA molecule.

In another embodiment, the invention features a method for synthesizing a siNA duplex molecule comprising: (a) synthesizing one oligonucleotide sequence strand of the siNA molecule, wherein the sequence comprises a cleavable linker molecule that can be used as a scaffold for the synthesis of another oligonucleotide sequence; (b) synthesizing a second oligonucleotide sequence having complementarity to the first sequence strand on the scaffold of (a), wherein the second sequence comprises the other strand of the double-stranded siNA molecule and wherein the second sequence further comprises a chemical moiety that can be used to isolate the attached oligonucleotide sequence; (c) purifying the product of (b) utilizing the chemical moiety of the second oligonucleotide sequence strand under conditions suitable for isolating the full-length sequence comprising both

siNA oligonucleotide strands connected by the cleavable linker and under conditions suitable for the two siNA oligonucleotide strands to hybridize and form a stable duplex. In one embodiment, cleavage of the linker molecule in (c) above takes place during deprotection of the oligonucleotide, for example under hydrolysis conditions. In another
5 embodiment, cleavage of the linker molecule in (c) above takes place after deprotection of the oligonucleotide. In another embodiment, the method of synthesis comprises solid phase synthesis on a solid support such as controlled pore glass (CPG) or polystyrene, wherein the first sequence of (a) is synthesized on a cleavable linker, such as a succinyl linker, using the solid support as a scaffold. The cleavable linker in (a) used as a scaffold
10 for synthesizing the second strand can comprise similar reactivity or differing reactivity as the solid support derivatized linker, such that cleavage of the solid support derivatized linker and the cleavable linker of (a) takes place either concomitantly or sequentially. In one embodiment, the chemical moiety of (b) that can be used to isolate the attached oligonucleotide sequence comprises a trityl group, for example a dimethoxytrityl group.

15 In another embodiment, the invention features a method for making a double-stranded siNA molecule in a single synthetic process comprising: (a) synthesizing an oligonucleotide having a first and a second sequence, wherein the first sequence is complementary to the second sequence, and the first oligonucleotide sequence is linked to the second sequence via a cleavable linker, and wherein a terminal 5'-protecting group,
20 for example, a 5'-O-dimethoxytrityl group (5'-O-DMT) remains on the oligonucleotide having the second sequence; (b) deprotecting the oligonucleotide whereby the deprotection results in the cleavage of the linker joining the two oligonucleotide sequences; and (c) purifying the product of (b) under conditions suitable for isolating the double-stranded siNA molecule, for example using a trityl-on synthesis strategy as
25 described herein.

In another embodiment, the method of synthesis of siNA molecules of the invention comprises the teachings of Scaringe *et al.*, US Patent Nos. 5,889,136; 6,008,400; and 6,111,086, incorporated by reference herein in their entirety.

30 In one embodiment, the invention features siNA constructs that mediate RNAi against PDGF and/or PDGFr, wherein the siNA construct comprises one or more chemical modifications, for example, one or more chemical modifications having any of

Formulae I-VII or any combination thereof that increases the nuclease resistance of the siNA construct.

In another embodiment, the invention features a method for generating siNA molecules with increased nuclease resistance comprising (a) introducing nucleotides
5 having any of Formula I-VII or any combination thereof into a siNA molecule, and (b) assaying the siNA molecule of step (a) under conditions suitable for isolating siNA molecules having increased nuclease resistance.

In one embodiment, the invention features siNA constructs that mediate RNAi against PDGF and/or PDGFr, wherein the siNA construct comprises one or more
10 chemical modifications described herein that modulates the binding affinity between the sense and antisense strands of the siNA construct.

In another embodiment, the invention features a method for generating siNA molecules with increased binding affinity between the sense and antisense strands of the siNA molecule comprising (a) introducing nucleotides having any of Formula I-VII or
15 any combination thereof into a siNA molecule, and (b) assaying the siNA molecule of step (a) under conditions suitable for isolating siNA molecules having increased binding affinity between the sense and antisense strands of the siNA molecule.

In one embodiment, the invention features siNA constructs that mediate RNAi against PDGF and/or PDGFr, wherein the siNA construct comprises one or more
20 chemical modifications described herein that modulates the binding affinity between the antisense strand of the siNA construct and a complementary target RNA sequence within a cell.

In one embodiment, the invention features siNA constructs that mediate RNAi against PDGF and/or PDGFr, wherein the siNA construct comprises one or more
25 chemical modifications described herein that modulates the binding affinity between the antisense strand of the siNA construct and a complementary target DNA sequence within a cell.

In another embodiment, the invention features a method for generating siNA molecules with increased binding affinity between the antisense strand of the siNA

molecule and a complementary target RNA sequence, comprising (a) introducing nucleotides having any of Formula I-VII or any combination thereof into a siNA molecule, and (b) assaying the siNA molecule of step (a) under conditions suitable for isolating siNA molecules having increased binding affinity between the antisense strand of the siNA molecule and a complementary target RNA sequence.

In another embodiment, the invention features a method for generating siNA molecules with increased binding affinity between the antisense strand of the siNA molecule and a complementary target DNA sequence, comprising (a) introducing nucleotides having any of Formula I-VII or any combination thereof into a siNA molecule, and (b) assaying the siNA molecule of step (a) under conditions suitable for isolating siNA molecules having increased binding affinity between the antisense strand of the siNA molecule and a complementary target DNA sequence.

In one embodiment, the invention features siNA constructs that mediate RNAi against PDGF and/or PDGFr, wherein the siNA construct comprises one or more chemical modifications described herein that modulate the polymerase activity of a cellular polymerase capable of generating additional endogenous siNA molecules having sequence homology to the chemically-modified siNA construct.

In another embodiment, the invention features a method for generating siNA molecules capable of mediating increased polymerase activity of a cellular polymerase capable of generating additional endogenous siNA molecules having sequence homology to a chemically-modified siNA molecule comprising (a) introducing nucleotides having any of Formula I-VII or any combination thereof into a siNA molecule, and (b) assaying the siNA molecule of step (a) under conditions suitable for isolating siNA molecules capable of mediating increased polymerase activity of a cellular polymerase capable of generating additional endogenous siNA molecules having sequence homology to the chemically-modified siNA molecule.

In one embodiment, the invention features chemically-modified siNA constructs that mediate RNAi against PDGF and/or PDGFr in a cell, wherein the chemical modifications do not significantly effect the interaction of siNA with a target RNA molecule, DNA molecule and/or proteins or other factors that are essential for RNAi in a manner that would decrease the efficacy of RNAi mediated by such siNA constructs.

In another embodiment, the invention features a method for generating siNA molecules with improved RNAi activity against PDGF and/or PDGFr comprising (a) introducing nucleotides having any of Formula I-VII or any combination thereof into a siNA molecule, and (b) assaying the siNA molecule of step (a) under conditions suitable for isolating siNA molecules having improved RNAi activity.

In yet another embodiment, the invention features a method for generating siNA molecules with improved RNAi activity against a PDGF and/or PDGFr target RNA comprising (a) introducing nucleotides having any of Formula I-VII or any combination thereof into a siNA molecule, and (b) assaying the siNA molecule of step (a) under conditions suitable for isolating siNA molecules having improved RNAi activity against the target RNA.

In yet another embodiment, the invention features a method for generating siNA molecules with improved RNAi activity against a PDGF and/or PDGFr target DNA, comprising (a) introducing nucleotides having any of Formula I-VII or any combination thereof into a siNA molecule, and (b) assaying the siNA molecule of step (a) under conditions suitable for isolating siNA molecules having improved RNAi activity against the target DNA.

In one embodiment, the invention features siNA constructs that mediate RNAi against PDGF and/or PDGFr, wherein the siNA construct comprises one or more chemical modifications described herein that modulates the cellular uptake of the siNA construct.

In another embodiment, the invention features a method for generating siNA molecules against PDGF and/or PDGFr with improved cellular uptake, comprising (a) introducing nucleotides having any of Formula I-VII or any combination thereof into a siNA molecule, and (b) assaying the siNA molecule of step (a) under conditions suitable for isolating siNA molecules having improved cellular uptake.

In one embodiment, the invention features siNA constructs that mediate RNAi against PDGF and/or PDGFr, wherein the siNA construct comprises one or more chemical modifications described herein that increases the bioavailability of the siNA construct, for example, by attaching polymeric conjugates such as polyethyleneglycol or

equivalent conjugates that improve the pharmacokinetics of the siNA construct, or by attaching conjugates that target specific tissue types or cell types *in vivo*. Non-limiting examples of such conjugates are described in Vargeese *et al.*, U.S. Serial No. 60/311,865 incorporated by reference herein.

5 In one embodiment, the invention features a method for generating siNA molecules of the invention with improved bioavailability, comprising (a) introducing a conjugate into the structure of a siNA molecule, and (b) assaying the siNA molecule of step (a) under conditions suitable for isolating siNA molecules having improved bioavailability. Such conjugates can include ligands for cellular receptors, such as peptides derived from
10 naturally occurring protein ligands; protein localization sequences, including cellular ZIP code sequences; antibodies; nucleic acid aptamers; vitamins; and other co-factors, such as folate and N-acetylgalactosamine; polymers, such as polyethyleneglycol (PEG); phospholipids; polyamines, such as spermine or spermidine; and others.

 In another embodiment, the invention features a method for generating siNA
15 molecules of the invention with improved bioavailability comprising (a) introducing an excipient formulation to a siNA molecule, and (b) assaying the siNA molecule of step (a) under conditions suitable for isolating siNA molecules having improved bioavailability. Such excipients include polymers such as cyclodextrins, lipids, cationic lipids, polyamines, phospholipids, and others.

20 In another embodiment, the invention features a method for generating siNA molecules of the invention with improved bioavailability comprising (a) introducing nucleotides having any of Formulae I-VII or any combination thereof into a siNA molecule, and (b) assaying the siNA molecule of step (a) under conditions suitable for isolating siNA molecules having improved bioavailability.

25 In another embodiment, polyethylene glycol (PEG) can be covalently attached to siNA compounds of the present invention. The attached PEG can be any molecular weight, preferably from about 2,000 to about 50,000 daltons (Da).

 The present invention can be used alone or as a component of a kit having at least one of the reagents necessary to carry out the *in vitro* or *in vivo* introduction of RNA to
30 test samples and/or subjects. For example, preferred components of the kit include the

siNA and a vehicle that promotes introduction of the siNA. Such a kit can also include instructions to allow a user of the kit to practice the invention.

The term "short interfering nucleic acid", "siNA", "short interfering RNA", "siRNA", "short interfering nucleic acid molecule", "short interfering oligonucleotide molecule", or "chemically-modified short interfering nucleic acid molecule" as used
5 herein refers to any nucleic acid molecule capable of mediating RNA interference "RNAi" or gene silencing in a sequence-specific manner; see for example Bass, 2001, *Nature*, 411, 428-429; Elbashir *et al.*, 2001, *Nature*, 411, 494-498; and Kreutzer *et al.*, International PCT Publication No. WO 00/44895; Zernicka-Goetz *et al.*, International
10 PCT Publication No. WO 01/36646; Fire, International PCT Publication No. WO 99/32619; Plaetinck *et al.*, International PCT Publication No. WO 00/01846; Mello and Fire, International PCT Publication No. WO 01/29058; Deschamps-Depaillette, International PCT Publication No. WO 99/07409; and Li *et al.*, International PCT
Publication No. WO 00/44914; Allshire, 2002, *Science*, 297, 1818-1819; Volpe *et al.*,
15 2002, *Science*, 297, 1833-1837; Jenuwein, 2002, *Science*, 297, 2215-2218; and Hall *et al.*, 2002, *Science*, 297, 2232-2237; Hutvagner and Zamore, 2002, *Science*, 297, 2056-60; McManus *et al.*, 2002, *RNA*, 8, 842-850; Reinhart *et al.*, 2002, *Gene & Dev.*, 16, 1616-1626; and Reinhart & Bartel, 2002, *Science*, 297, 1831). Non limiting examples of siNA molecules of the invention are shown in **Figures 4-6**, and **Tables II, III, and IV** herein.
20 For example the siNA can be a double-stranded polynucleotide molecule comprising self-complementary sense and antisense regions, wherein the antisense region comprises nucleotide sequence that is complementary to nucleotide sequence in a target nucleic acid molecule or a portion thereof and the sense region having nucleotide sequence corresponding to the target nucleic acid sequence or a portion thereof. The siNA can be
25 assembled from two separate oligonucleotides, where one strand is the sense strand and the other is the antisense strand, wherein the antisense and sense strands are self-complementary (i.e. each strand comprises nucleotide sequence that is complementary to nucleotide sequence in the other strand); the antisense strand comprises nucleotide sequence that is complementary to nucleotide sequence in a target nucleic acid molecule
30 or a portion thereof and the sense strand comprises nucleotide sequence corresponding to the target nucleic acid sequence or a portion thereof. Alternatively, the siNA is assembled from a single oligonucleotide, where the self-complementary sense and

antisense regions of the siNA are linked by means of a nucleic acid based or non-nucleic acid-based linker(s). The siNA can be a polynucleotide with a hairpin secondary structure, having self-complementary sense and antisense regions, wherein the antisense region comprises nucleotide sequence that is complementary to nucleotide sequence in a
5 separate target nucleic acid molecule or a portion thereof and the sense region having nucleotide sequence corresponding to the target nucleic acid sequence or a portion thereof. The siNA can be a circular single-stranded polynucleotide having two or more loop structures and a stem comprising self-complementary sense and antisense regions, wherein the antisense region comprises nucleotide sequence that is complementary to
10 nucleotide sequence in a target nucleic acid molecule or a portion thereof and the sense region having nucleotide sequence corresponding to the target nucleic acid sequence or a portion thereof, and wherein the circular polynucleotide can be processed either *in vivo* or *in vitro* to generate an active siNA molecule capable of mediating RNAi. The siNA can also comprise a single stranded polynucleotide having nucleotide sequence
15 complementary to nucleotide sequence in a target nucleic acid molecule or a portion thereof (for example, where such siNA molecule does not require the presence within the siNA molecule of nucleotide sequence corresponding to the target nucleic acid sequence or a portion thereof), wherein the single stranded polynucleotide can further comprise a terminal phosphate group, such as a 5'-phosphate (see for example Martinez *et al.*, 2002, *Cell*, 110, 563-574 and Schwarz *et al.*, 2002, *Molecular Cell*, 10, 537-568), or 5',3'-diphosphate. In certain embodiments, the siNA molecules of the invention comprise nucleotide sequence that is complementary to nucleotide sequence of a target gene. In another embodiment, the siNA molecule of the invention interacts with nucleotide sequence of a target gene in a manner that causes inhibition of expression of the target
25 gene. As used herein, siNA molecules need not be limited to those molecules containing only RNA, but further encompasses chemically-modified nucleotides and non-nucleotides. In certain embodiments, the short interfering nucleic acid molecules of the invention lack 2'-hydroxy (2'-OH) containing nucleotides. Applicant describes in certain embodiments short interfering nucleic acids that do not require the presence of
30 nucleotides having a 2'-hydroxy group for mediating RNAi and as such, short interfering nucleic acid molecules of the invention optionally do not include any ribonucleotides (e.g., nucleotides having a 2'-OH group). Such siNA molecules that do not require the presence of ribonucleotides within the siNA molecule to support RNAi can however have

an attached linker or linkers or other attached or associated groups, moieties, or chains containing one or more nucleotides with 2'-OH groups. Optionally, siNA molecules can comprise ribonucleotides at about 5, 10, 20, 30, 40, or 50% of the nucleotide positions. The modified short interfering nucleic acid molecules of the invention can also be referred to as short interfering modified oligonucleotides "'siMON." As used herein, the term siNA is meant to be equivalent to other terms used to describe nucleic acid molecules that are capable of mediating sequence specific RNAi, for example short interfering RNA (siRNA), double-stranded RNA (dsRNA), micro-RNA (miRNA), short hairpin RNA (shRNA), short interfering oligonucleotide, short interfering nucleic acid, short interfering modified oligonucleotide, chemically-modified siRNA, post-transcriptional gene silencing RNA (ptgsRNA), and others. In addition, as used herein, the term RNAi is meant to be equivalent to other terms used to describe sequence specific RNA interference, such as post transcriptional gene silencing, or epigenetics. For example, siNA molecules of the invention can be used to epigenetically silence genes at both the post-transcriptional level or the pre-transcriptional level. In a non-limiting example, epigenetic regulation of gene expression by siNA molecules of the invention can result from siNA mediated modification of chromatin structure to alter gene expression (see, for example, Allshire, 2002, *Science*, 297, 1818-1819; Volpe *et al.*, 2002, *Science*, 297, 1833-1837; Jenuwein, 2002, *Science*, 297, 2215-2218; and Hall *et al.*, 2002, *Science*, 297, 2232-2237).

By "modulate" is meant that the expression of the gene, or level of RNA molecule or equivalent RNA molecules encoding one or more proteins or protein subunits, or activity of one or more proteins or protein subunits is up regulated or down regulated, such that expression, level, or activity is greater than or less than that observed in the absence of the modulator. For example, the term "modulate" can mean "inhibit," but the use of the word "modulate" is not limited to this definition.

By "inhibit" it is meant that the activity of a gene expression product or level of RNAs or equivalent RNAs encoding one or more gene products is reduced below that observed in the absence of the nucleic acid molecule of the invention. In one embodiment, inhibition with a siNA molecule preferably is below that level observed in the presence of an inactive or attenuated molecule that is unable to mediate an RNAi response. In another embodiment, inhibition of gene expression with the siNA molecule

of the instant invention is greater in the presence of the siNA molecule than in its absence.

By "gene" or "target gene" is meant, a nucleic acid that encodes an RNA, for example, nucleic acid sequences including, but not limited to, structural genes encoding a polypeptide. The target gene can be a gene derived from a cell, an endogenous gene, a transgene, or exogenous genes such as genes of a pathogen, for example a virus, which is present in the cell after infection thereof. The cell containing the target gene can be derived from or contained in any organism, for example a plant, animal, protozoan, virus, bacterium, or fungus. Non-limiting examples of plants include monocots, dicots, or gymnosperms. Non-limiting examples of animals include vertebrates or invertebrates. Non-limiting examples of fungi include molds or yeasts.

By "PDGF" is meant, any platelet derived growth factor polypeptide, protein and/or a polynucleotide encoding a platelet derived growth factor protein, peptide, or portion thereof (such as polynucleotides referred to by Genbank Accession numbers in **Table I** or any other platelet derived growth factor transcript derived from a PDGF gene).

By "PDGFr" is meant, any platelet derived growth factor receptor polypeptide, protein and/or a polynucleotide encoding a platelet derived growth factor receptor protein, peptide, or portion thereof (such as polynucleotides referred to by Genbank Accession numbers in **Table I** or any other platelet derived growth factor transcript derived from a PDGFr gene).

By "PDGF protein" is meant, any platelet derived growth factor peptide or protein or a component thereof, wherein the peptide or protein is encoded by a PDGF gene or having platelet derived growth factor activity.

By "PDGFr protein" is meant, any platelet derived growth factor receptor peptide or protein or a component thereof, wherein the peptide or protein is encoded by a PDGFr gene or having platelet derived growth factor receptor activity.

By "highly conserved sequence region" is meant, a nucleotide sequence of one or more regions in a target gene does not vary significantly from one generation to the other or from one biological system to the other.

By "sense region" is meant a nucleotide sequence of a siNA molecule having complementarity to an antisense region of the siNA molecule. In addition, the sense region of a siNA molecule can comprise a nucleic acid sequence having homology with a target nucleic acid sequence.

5 By "antisense region" is meant a nucleotide sequence of a siNA molecule having complementarity to a target nucleic acid sequence. In addition, the antisense region of a siNA molecule can optionally comprise a nucleic acid sequence having complementarity to a sense region of the siNA molecule.

10 By "target nucleic acid" is meant any nucleic acid sequence whose expression or activity is to be modulated. The target nucleic acid can be DNA or RNA.

By "complementarity" is meant that a nucleic acid can form hydrogen bond(s) with another nucleic acid sequence by either traditional Watson-Crick or other non-traditional types. In reference to the nucleic molecules of the present invention, the binding free energy for a nucleic acid molecule with its complementary sequence is sufficient to allow the relevant function of the nucleic acid to proceed, e.g., RNAi activity. Determination of binding free energies for nucleic acid molecules is well known in the art (see, e.g., Turner *et al.*, 1987, *CSH Symp. Quant. Biol.* LII pp.123-133; Frier *et al.*, 1986, *Proc. Nat. Acad. Sci. USA* 83:9373-9377; Turner *et al.*, 1987, *J. Am. Chem. Soc.* 109:3783-3785). A percent complementarity indicates the percentage of contiguous residues in a nucleic acid molecule that can form hydrogen bonds (e.g., Watson-Crick base pairing) with a second nucleic acid sequence (e.g., 5, 6, 7, 8, 9, 10 out of 10 being 50%, 60%, 70%, 80%, 90%, and 100% complementary). "Perfectly complementary" means that all the contiguous residues of a nucleic acid sequence will hydrogen bond with the same number of contiguous residues in a second nucleic acid sequence.

25 The siNA molecules of the invention represent a novel therapeutic approach to treat a variety of oncogenic and proliferative diseases and disorders including various cancers including but not limited to multiple drug resistant cancers, such as leukemias including acute myelogenous leukemia (AML), chronic myelogenous leukemia (CML), Acute lymphocytic leukemia (ALL), and chronic lymphocytic leukemia; ovarian cancer, breast cancer, cancers of the head and neck, lymphomas such as mantle cell lymphoma, non-Hodgkin's lymphoma, Burkitt's lymphoma, adenoma, squamous cell carcinoma,

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laryngeal carcinoma, multiple myeloma, melanoma, colorectal cancer, prostate cancer; and proliferative diseases such as restenosis, polycystic kidney disease and any other indications that can respond to the level of PDGF and/or PDGFr in a cell or tissue..

In one embodiment of the present invention, each sequence of a siNA molecule of the invention is independently about 18 to about 24 nucleotides in length, in specific embodiments about 18, 19, 20, 21, 22, 23, or 24 nucleotides in length. In another embodiment, the siNA duplexes of the invention independently comprise about 17 to about 23 base pairs (*e.g.*, about 17, 18, 19, 20, 21, 22 or 23). In yet another embodiment, siNA molecules of the invention comprising hairpin or circular structures are about 35 to about 55 (*e.g.*, about 35, 40, 45, 50 or 55) nucleotides in length, or about 38 to about 44 (*e.g.*, 38, 39, 40, 41, 42, 43 or 44) nucleotides in length and comprising about 16 to about 22 (*e.g.*, about 16, 17, 18, 19, 20, 21 or 22) base pairs. Exemplary siNA molecules of the invention are shown in **Table II**. Exemplary synthetic siNA molecules of the invention are shown in **Tables III and IV** and/or **Figures 4-5**.

As used herein "cell" is used in its usual biological sense, and does not refer to an entire multicellular organism, *e.g.*, specifically does not refer to a human. The cell can be present in an organism, *e.g.*, birds, plants and mammals such as humans, cows, sheep, apes, monkeys, swine, dogs, and cats. The cell can be prokaryotic (*e.g.*, bacterial cell) or eukaryotic (*e.g.*, mammalian or plant cell). The cell can be of somatic or germ line origin, totipotent or pluripotent, dividing or non-dividing. The cell can also be derived from or can comprise a gamete or embryo, a stem cell, or a fully differentiated cell.

The siNA molecules of the invention are added directly, or can be complexed with cationic lipids, packaged within liposomes, or otherwise delivered to target cells or tissues. The nucleic acid or nucleic acid complexes can be locally administered to relevant tissues *ex vivo*, or *in vivo* through injection, infusion pump or stent, with or without their incorporation in biopolymers. In particular embodiments, the nucleic acid molecules of the invention comprise sequences shown in **Tables II-III** and/or **Figures 4-5**. Examples of such nucleic acid molecules consist essentially of sequences defined in these tables and figures. Furthermore, the chemical modification constructs described in **Table IV** can be applied to any siNA sequence of the invention.

In another aspect, the invention provides mammalian cells containing one or more siNA molecules of this invention. The one or more siNA molecules can independently be targeted to the same or different sites.

By "RNA" is meant a molecule comprising at least one ribonucleotide residue. By
5 "ribonucleotide" is meant a nucleotide with a hydroxyl group at the 2' position of a β -D-ribo-furanose moiety. The terms include double-stranded RNA, single-stranded RNA, isolated RNA such as partially purified RNA, essentially pure RNA, synthetic RNA, recombinantly produced RNA, as well as altered RNA that differs from naturally
10 occurring RNA by the addition, deletion, substitution and/or alteration of one or more nucleotides. Such alterations can include addition of non-nucleotide material, such as to the end(s) of the siNA or internally, for example at one or more nucleotides of the RNA. Nucleotides in the RNA molecules of the instant invention can also comprise non-standard nucleotides, such as non-naturally occurring nucleotides or chemically
15 synthesized nucleotides or deoxynucleotides. These altered RNAs can be referred to as analogs or analogs of naturally-occurring RNA.

By "subject" is meant an organism, which is a donor or recipient of explanted cells or the cells themselves. "Subject" also refers to an organism to which the nucleic acid molecules of the invention can be administered. In one embodiment, a subject is a mammal or mammalian cells. In another embodiment, a subject is a human or human
20 cells.

The term "phosphorothioate" as used herein refers to an internucleotide linkage having Formula I, wherein Z and/or W comprise a sulfur atom. Hence, the term phosphorothioate refers to both phosphorothioate and phosphorodithioate internucleotide linkages.

25 The term "universal base" as used herein refers to nucleotide base analogs that form base pairs with each of the natural DNA/RNA bases with little discrimination between them. Non-limiting examples of universal bases include C-phenyl, C-naphthyl and other aromatic derivatives, inosine, azole carboxamides, and nitroazole derivatives such as 3-nitropyrrole, 4-nitroindole, 5-nitroindole, and 6-nitroindole as known in the art (see for
30 example Loakes, 2001, *Nucleic Acids Research*, 29, 2437-2447).

The term "acyclic nucleotide" as used herein refers to any nucleotide having an acyclic ribose sugar, for example where any of the ribose carbons (C1, C2, C3, C4, or C5), are independently or in combination absent from the nucleotide.

The nucleic acid molecules of the instant invention, individually, or in combination
5 or in conjunction with other drugs, can be used to treat diseases or conditions discussed herein (e.g., cancers and other proliferative conditions). For example, to treat a particular disease or condition, the siNA molecules can be administered to a subject or can be administered to other appropriate cells evident to those skilled in the art, individually or in combination with one or more drugs under conditions suitable for the treatment.

10 In a further embodiment, the siNA molecules can be used in combination with other known treatments to treat conditions or diseases discussed above. For example, the described molecules could be used in combination with one or more known therapeutic agents to treat a disease or condition. Non-limiting examples of other therapeutic agents that can be readily combined with a siNA molecule of the invention are enzymatic nucleic
15 acid molecules, allosteric nucleic acid molecules, antisense, decoy, or aptamer nucleic acid molecules, antibodies such as monoclonal antibodies, small molecules, and other organic and/or inorganic compounds including metals, salts and ions.

In one embodiment, the invention features an expression vector comprising a nucleic acid sequence encoding at least one siNA molecule of the invention, in a manner
20 which allows expression of the siNA molecule. For example, the vector can contain sequence(s) encoding both strands of a siNA molecule comprising a duplex. The vector can also contain sequence(s) encoding a single nucleic acid molecule that is self-complementary and thus forms a siNA molecule. Non-limiting examples of such expression vectors are described in Paul *et al.*, 2002, *Nature Biotechnology*, 19, 505;
25 Miyagishi and Taira, 2002, *Nature Biotechnology*, 19, 497; Lee *et al.*, 2002, *Nature Biotechnology*, 19, 500; and Novina *et al.*, 2002, *Nature Medicine*, advance online publication doi:10.1038/nm725.

In another embodiment, the invention features a mammalian cell, for example, a human cell, including an expression vector of the invention.

In yet another embodiment, the expression vector of the invention comprises a sequence for a siNA molecule having complementarity to a RNA molecule referred to by a Genbank Accession numbers, for example Genbank Accession Nos. shown in **Table I**.

5 In one embodiment, an expression vector of the invention comprises a nucleic acid sequence encoding two or more siNA molecules, which can be the same or different.

In another aspect of the invention, siNA molecules that interact with target RNA molecules and down-regulate gene encoding target RNA molecules (for example target RNA molecules referred to by Genbank Accession numbers herein) are expressed from transcription units inserted into DNA or RNA vectors. The recombinant vectors can be
10 DNA plasmids or viral vectors. siNA expressing viral vectors can be constructed based on, but not limited to, adeno-associated virus, retrovirus, adenovirus, or alphavirus. The recombinant vectors capable of expressing the siNA molecules can be delivered as described herein, and persist in target cells. Alternatively, viral vectors can be used that provide for transient expression of siNA molecules. Such vectors can be repeatedly
15 administered as necessary. Once expressed, the siNA molecules bind and down-regulate gene function or expression via RNA interference (RNAi). Delivery of siNA expressing vectors can be systemic, such as by intravenous or intramuscular administration, by administration to target cells ex-planted from a subject followed by reintroduction into the subject, or by any other means that would allow for introduction into the desired target
20 cell.

By "vectors" is meant any nucleic acid- and/or viral-based technique used to deliver a desired nucleic acid.

Other features and advantages of the invention will be apparent from the following description of the preferred embodiments thereof, and from the claims.

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BRIEF DESCRIPTION OF THE DRAWINGS

Figure 1 shows a non-limiting example of a scheme for the synthesis of siNA molecules. The complementary siNA sequence strands, strand 1 and strand 2, are synthesized in tandem and are connected by a cleavable linkage, such as a nucleotide succinate or abasic succinate, which can be the same or different from the cleavable

linker used for solid phase synthesis on a solid support. The synthesis can be either solid phase or solution phase, in the example shown, the synthesis is a solid phase synthesis. The synthesis is performed such that a protecting group, such as a dimethoxytrityl group, remains intact on the terminal nucleotide of the tandem oligonucleotide. Upon cleavage and deprotection of the oligonucleotide, the two siNA strands spontaneously hybridize to form a siNA duplex, which allows the purification of the duplex by utilizing the properties of the terminal protecting group, for example by applying a trityl on purification method wherein only duplexes/oligonucleotides with the terminal protecting group are isolated.

Figure 2 shows a MALDI-TOV mass spectrum of a purified siNA duplex synthesized by a method of the invention. The two peaks shown correspond to the predicted mass of the separate siNA sequence strands. This result demonstrates that the siNA duplex generated from tandem synthesis can be purified as a single entity using a simple trityl-on purification methodology.

Figure 3 shows a non-limiting proposed mechanistic representation of target RNA degradation involved in RNAi. Double-stranded RNA (dsRNA), which is generated by RNA-dependent RNA polymerase (RdRP) from foreign single-stranded RNA, for example viral, transposon, or other exogenous RNA, activates the DICER enzyme that in turn generates siNA duplexes. Alternately, synthetic or expressed siNA can be introduced directly into a cell by appropriate means. An active siNA complex forms which recognizes a target RNA, resulting in degradation of the target RNA by the RISC endonuclease complex or in the synthesis of additional RNA by RNA-dependent RNA polymerase (RdRP), which can activate DICER and result in additional siNA molecules, thereby amplifying the RNAi response.

Figure 4A-F shows non-limiting examples of chemically-modified siNA constructs of the present invention. In the figure, N stands for any nucleotide (adenosine, guanosine, cytosine, uridine, or optionally thymidine, for example thymidine can be substituted in the overhanging regions designated by parenthesis (N N). Various modifications are shown for the sense and antisense strands of the siNA constructs.

Figure 4A: The sense strand comprises 21 nucleotides having four phosphorothioate 5'- and 3'-terminal internucleotide linkages, wherein the two terminal 3'-

nucleotides are optionally base paired and wherein all pyrimidine nucleotides that may be present are 2'-O-methyl or 2'-deoxy-2'-fluoro modified nucleotides except for (N N) nucleotides, which can comprise ribonucleotides, deoxynucleotides, universal bases, or other chemical modifications described herein. The antisense strand comprises 21
5 nucleotides, optionally having a 3'-terminal glyceryl moiety and wherein the two terminal 3'-nucleotides are optionally complementary to the target RNA sequence, and having one 3'-terminal phosphorothioate internucleotide linkage and four 5'-terminal phosphorothioate internucleotide linkages and wherein all pyrimidine nucleotides that may be present are 2'-deoxy-2'-fluoro modified nucleotides except for (N N) nucleotides,
10 which can comprise ribonucleotides, deoxynucleotides, universal bases, or other chemical modifications described herein.

Figure 4B: The sense strand comprises 21 nucleotides wherein the two terminal 3'-nucleotides are optionally base paired and wherein all pyrimidine nucleotides that may be present are 2'-O-methyl or 2'-deoxy-2'-fluoro modified nucleotides except for (N N)
15 nucleotides, which can comprise ribonucleotides, deoxynucleotides, universal bases, or other chemical modifications described herein. The antisense strand comprises 21 nucleotides, optionally having a 3'-terminal glyceryl moiety and wherein the two terminal 3'-nucleotides are optionally complementary to the target RNA sequence, and wherein all pyrimidine nucleotides that may be present are 2'-deoxy-2'-fluoro modified nucleotides
20 except for (N N) nucleotides, which can comprise ribonucleotides, deoxynucleotides, universal bases, or other chemical modifications described herein.

Figure 4C: The sense strand comprises 21 nucleotides having 5'- and 3'- terminal cap moieties wherein the two terminal 3'-nucleotides are optionally base paired and wherein all pyrimidine nucleotides that may be present are 2'-O-methyl or 2'-deoxy-2'-
25 fluoro modified nucleotides except for (N N) nucleotides, which can comprise ribonucleotides, deoxynucleotides, universal bases, or other chemical modifications described herein. The antisense strand comprises 21 nucleotides, optionally having a 3'-terminal glyceryl moiety and wherein the two terminal 3'-nucleotides are optionally complementary to the target RNA sequence, and having one 3'-terminal phosphorothioate
30 internucleotide linkage and wherein all pyrimidine nucleotides that may be present are 2'-deoxy-2'-fluoro modified nucleotides except for (N N) nucleotides, which can comprise

ribonucleotides, deoxynucleotides, universal bases, or other chemical modifications described herein.

Figure 4D: The sense strand comprises 21 nucleotides having 5'- and 3'- terminal cap moieties wherein the two terminal 3'-nucleotides are optionally base paired and wherein all pyrimidine nucleotides that may be present are 2'-deoxy-2'-fluoro modified nucleotides except for (N N) nucleotides, which can comprise ribonucleotides, deoxynucleotides, universal bases, or other chemical modifications described herein and wherein all purine nucleotides that may be present are 2'-deoxy nucleotides. The antisense strand comprises 21 nucleotides, optionally having a 3'-terminal glyceryl moiety and wherein the two terminal 3'-nucleotides are optionally complementary to the target RNA sequence, and having one 3'-terminal phosphorothioate internucleotide linkage and wherein all pyrimidine nucleotides that may be present are 2'-deoxy-2'-fluoro modified nucleotides and all purine nucleotides that may be present are 2'-O-methyl modified nucleotides except for (N N) nucleotides, which can comprise ribonucleotides, deoxynucleotides, universal bases, or other chemical modifications described herein.

Figure 4E: The sense strand comprises 21 nucleotides having 5'- and 3'- terminal cap moieties wherein the two terminal 3'-nucleotides are optionally base paired and wherein all pyrimidine nucleotides that may be present are 2'-deoxy-2'-fluoro modified nucleotides except for (N N) nucleotides, which can comprise ribonucleotides, deoxynucleotides, universal bases, or other chemical modifications described herein. The antisense strand comprises 21 nucleotides, optionally having a 3'-terminal glyceryl moiety and wherein the two terminal 3'-nucleotides are optionally complementary to the target RNA sequence, and wherein all pyrimidine nucleotides that may be present are 2'-deoxy-2'-fluoro modified nucleotides and all purine nucleotides that may be present are 2'-O-methyl modified nucleotides except for (N N) nucleotides, which can comprise ribonucleotides, deoxynucleotides, universal bases, or other chemical modifications described herein.

Figure 4F: The sense strand comprises 21 nucleotides having 5'- and 3'- terminal cap moieties wherein the two terminal 3'-nucleotides are optionally base paired and wherein all pyrimidine nucleotides that may be present are 2'-deoxy-2'-fluoro modified nucleotides except for (N N) nucleotides, which can comprise ribonucleotides,

deoxynucleotides, universal bases, or other chemical modifications described herein. The antisense strand comprises 21 nucleotides, optionally having a 3'-terminal glyceryl moiety and wherein the two terminal 3'-nucleotides are optionally complementary to the target RNA sequence, and having one 3'-terminal phosphorothioate internucleotide linkage and
5 wherein all pyrimidine nucleotides that may be present are 2'-deoxy-2'-fluoro modified nucleotides and all purine nucleotides that may be present are 2'-deoxy nucleotides except for (N N) nucleotides, which can comprise ribonucleotides, deoxynucleotides, universal bases, or other chemical modifications described herein. The antisense strand of constructs A-F comprise sequence complementary to any target nucleic acid sequence of
10 the invention.

Figure 5A-F shows non-limiting examples of specific chemically-modified siNA sequences of the invention. **A-F** applies the chemical modifications described in **Figure 4A-F** to a PDGFr siNA sequence.

Figure 6 shows non-limiting examples of different siNA constructs of the
15 invention. The examples shown (constructs 1, 2, and 3) have 19 representative base pairs; however, different embodiments of the invention include any number of base pairs described herein. Bracketed regions represent nucleotide overhangs, for example comprising about 1, 2, 3, or 4 nucleotides in length, preferably about 2 nucleotides. Constructs 1 and 2 can be used independently for RNAi activity. Construct 2 can
20 comprise a polynucleotide or non-nucleotide linker, which can optionally be designed as a biodegradable linker. In one embodiment, the loop structure shown in construct 2 can comprise a biodegradable linker that results in the formation of construct 1 *in vivo* and/or *in vitro*. In another example, construct 3 can be used to generate construct 2 under the same principle wherein a linker is used to generate the active siNA construct 2 *in vivo*
25 and/or *in vitro*, which can optionally utilize another biodegradable linker to generate the active siNA construct 1 *in vivo* and/or *in vitro*. As such, the stability and/or activity of the siNA constructs can be modulated based on the design of the siNA construct for use *in vivo* or *in vitro* and/or *in vitro*.

Figure 7A-C is a diagrammatic representation of a scheme utilized in generating an
30 expression cassette to generate siNA hairpin constructs.

Figure 7A: A DNA oligomer is synthesized with a 5'-restriction site (R1) sequence followed by a region having sequence identical (sense region of siNA) to a predetermined PDGF and/or PDGFr target sequence, wherein the sense region comprises, for example, about 19, 20, 21, or 22 nucleotides (N) in length, which is followed by a loop sequence of defined sequence (X), comprising, for example, about 3 to about 10 nucleotides.

Figure 7B: The synthetic construct is then extended by DNA polymerase to generate a hairpin structure having self-complementary sequence that will result in a siNA transcript having specificity for a PDGF and/or PDGFr target sequence and having self-complementary sense and antisense regions.

Figure 7C: The construct is heated (for example to about 95°C) to linearize the sequence, thus allowing extension of a complementary second DNA strand using a primer to the 3'-restriction sequence of the first strand. The double-stranded DNA is then inserted into an appropriate vector for expression in cells. The construct can be designed such that a 3'-terminal nucleotide overhang results from the transcription, for example by engineering restriction sites and/or utilizing a poly-U termination region as described in Paul *et al.*, 2002, *Nature Biotechnology*, 29, 505-508.

Figure 8A-C is a diagrammatic representation of a scheme utilized in generating an expression cassette to generate double-stranded siNA constructs.

Figure 8A: A DNA oligomer is synthesized with a 5'-restriction (R1) site sequence followed by a region having sequence identical (sense region of siNA) to a predetermined PDGF and/or PDGFr target sequence, wherein the sense region comprises, for example, about 19, 20, 21, or 22 nucleotides (N) in length, and which is followed by a 3'-restriction site (R2) which is adjacent to a loop sequence of defined sequence (X).

Figure 8B: The synthetic construct is then extended by DNA polymerase to generate a hairpin structure having self-complementary sequence.

Figure 8C: The construct is processed by restriction enzymes specific to R1 and R2 to generate a double-stranded DNA which is then inserted into an appropriate vector for expression in cells. The transcription cassette is designed such that a U6 promoter region

flanks each side of the dsDNA which generates the separate sense and antisense strands of the siNA. Poly T termination sequences can be added to the constructs to generate U overhangs in the resulting transcript.

Figure 9A-E is a diagrammatic representation of a method used to determine target sites for siNA mediated RNAi within a particular target nucleic acid sequence, such as messenger RNA.

Figure 9A: A pool of siNA oligonucleotides are synthesized wherein the antisense region of the siNA constructs has complementarity to target sites across the target nucleic acid sequence, and wherein the sense region comprises sequence complementary to the antisense region of the siNA.

Figure 9B&C: (Figure 9B) The sequences are pooled and are inserted into vectors such that **(Figure 9C)** transfection of a vector into cells results in the expression of the siNA.

Figure 9D: Cells are sorted based on phenotypic change that is associated with modulation of the target nucleic acid sequence.

Figure 9E: The siNA is isolated from the sorted cells and is sequenced to identify efficacious target sites within the target nucleic acid sequence.

Figure 10 shows non-limiting examples of different stabilization chemistries (1-10) that can be used, for example, to stabilize the 3'-end of siNA sequences of the invention, including (1) [3-3']-inverted deoxyribose; (2) deoxyribonucleotide; (3) [5'-3']-3'-deoxyribonucleotide; (4) [5'-3']-ribonucleotide; (5) [5'-3']-3'-O-methyl ribonucleotide; (6) 3'-glyceryl; (7) [3'-5']-3'-deoxyribonucleotide; (8) [3'-3']-deoxyribonucleotide; (9) [5'-2']-deoxyribonucleotide; and (10) [5-3']-dideoxyribonucleotide. In addition to modified and unmodified backbone chemistries indicated in the figure, these chemistries can be combined with different backbone modifications as described herein, for example, backbone modifications having Formula I. In addition, the 2'-deoxy nucleotide shown 5' to the terminal modifications shown can be another modified or unmodified nucleotide or non-nucleotide described herein, for example modifications having any of Formulae I-VII or any combination thereof.

Figure 11 shows a non-limiting example of a strategy used to identify chemically modified siNA constructs of the invention that are nuclease resistance while preserving the ability to mediate RNAi activity. Chemical modifications are introduced into the siNA construct based on “educated” design parameters (e.g. introducing 2’-mofications, base modifications, backbone modifications, terminal cap modifications etc). The modified construct is tested in an appropriate system (e.g. human serum for nuclease resistance, shown, or an animal model for PK/delivery parameters). In parallel, the siNA construct is tested for RNAi activity, for example in a cell culture system such as a luciferase reporter assay). Lead siNA constructs are then identified which possess a particular characteristic while maintaining RNAi activity, and can be further modified and assayed once again. This same approach can be used to identify siNA-conjugate molecules with improved pharmacokinetic profiles, delivery, and RNAi activity.

DETAILED DESCRIPTION OF THE INVENTION

Mechanism of action of Nucleic Acid Molecules of the Invention

The discussion that follows discusses the proposed mechanism of RNA interference mediated by short interfering RNA as is presently known, and is not meant to be limiting and is not an admission of prior art. Applicant demonstrates herein that chemically-modified short interfering nucleic acids possess similar or improved capacity to mediate RNAi as do siRNA molecules and are expected to possess improved stability and activity *in vivo*; therefore, this discussion is not meant to be limiting only to siRNA and can be applied to siNA as a whole. By “improved capacity to mediate RNAi” or “improved RNAi activity” is meant to include RNAi activity measured *in vitro* and/or *in vivo* where the RNAi activity is a reflection of both the ability of the siNA to mediate RNAi and the stability of the siNAs of the invention. In this invention, the product of these activities can be increased *in vitro* and/or *in vivo* compared to an all RNA siRNA or a siNA containing a plurality of ribonucleotides. In some cases, the activity or stability of the siNA molecule can be decreased (i.e., less than ten-fold), but the overall activity of the siNA molecule is enhanced *in vitro* and/or *in vivo*.

RNA interference refers to the process of sequence specific post-transcriptional gene silencing in animals mediated by short interfering RNAs (siRNAs) (Fire *et al.*, 1998, *Nature*, 391, 806). The corresponding process in plants is commonly referred to as post-

transcriptional gene silencing or RNA silencing and is also referred to as quelling in fungi. The process of post-transcriptional gene silencing is thought to be an evolutionarily-conserved cellular defense mechanism used to prevent the expression of foreign genes which is commonly shared by diverse flora and phyla (Fire *et al.*, 1999, *Trends Genet.*, 15, 358). Such protection from foreign gene expression may have evolved in response to the production of double-stranded RNAs (dsRNAs) derived from viral infection or the random integration of transposon elements into a host genome via a cellular response that specifically destroys homologous single-stranded RNA or viral genomic RNA. The presence of dsRNA in cells triggers the RNAi response through a mechanism that has yet to be fully characterized. This mechanism appears to be different from the interferon response that results from dsRNA-mediated activation of protein kinase PKR and 2', 5'-oligoadenylate synthetase resulting in non-specific cleavage of mRNA by ribonuclease L.

The presence of long dsRNAs in cells stimulates the activity of a ribonuclease III enzyme referred to as Dicer. Dicer is involved in the processing of the dsRNA into short pieces of dsRNA known as short interfering RNAs (siRNAs) (Berstein *et al.*, 2001, *Nature*, 409, 363). Short interfering RNAs derived from Dicer activity are typically about 21 to about 23 nucleotides in length and comprise about 19 base pair duplexes. Dicer has also been implicated in the excision of 21- and 22-nucleotide small temporal RNAs (stRNAs) from precursor RNA of conserved structure that are implicated in translational control (Hutvagner *et al.*, 2001, *Science*, 293, 834). The RNAi response also features an endonuclease complex containing a siRNA, commonly referred to as an RNA-induced silencing complex (RISC), which mediates cleavage of single-stranded RNA having sequence homologous to the siRNA. Cleavage of the target RNA takes place in the middle of the region complementary to the guide sequence of the siRNA duplex (Elbashir *et al.*, 2001, *Genes Dev.*, 15, 188). In addition, RNA interference can also involve small RNA (e.g., micro-RNA or miRNA) mediated gene silencing, presumably through cellular mechanisms that regulate chromatin structure and thereby prevent transcription of target gene sequences (see for example Allshire, 2002, *Science*, 297, 1818-1819; Volpe *et al.*, 2002, *Science*, 297, 1833-1837; Jenuwein, 2002, *Science*, 297, 2215-2218; and Hall *et al.*, 2002, *Science*, 297, 2232-2237). As such, siRNA molecules of the invention can be used to mediate gene silencing via interaction with RNA transcripts or alternately by interaction

with particular gene sequences, wherein such interaction results in gene silencing either at the transcriptional level or post-transcriptional level.

RNAi has been studied in a variety of systems. Fire *et al.*, 1998, *Nature*, 391, 806, were the first to observe RNAi in *C. elegans*. Wianny and Goetz, 1999, *Nature Cell Biol.*, 2, 70, describe RNAi mediated by dsRNA in mouse embryos. Hammond *et al.*, 2000, *Nature*, 404, 293, describe RNAi in *Drosophila* cells transfected with dsRNA. Elbashir *et al.*, 2001, *Nature*, 411, 494, describe RNAi induced by introduction of duplexes of synthetic 21-nucleotide RNAs in cultured mammalian cells including human embryonic kidney and HeLa cells. Recent work in *Drosophila* embryonic lysates has revealed certain requirements for siRNA length, structure, chemical composition, and sequence that are essential to mediate efficient RNAi activity. These studies have shown that 21 nucleotide siRNA duplexes are most active when containing two 2-nucleotide 3'-terminal nucleotide overhangs. Furthermore, substitution of one or both siRNA strands with 2'-deoxy or 2'-O-methyl nucleotides abolishes RNAi activity, whereas substitution of 3'-terminal siRNA nucleotides with deoxy nucleotides was shown to be tolerated. Mismatch sequences in the center of the siRNA duplex were also shown to abolish RNAi activity. In addition, these studies also indicate that the position of the cleavage site in the target RNA is defined by the 5'-end of the siRNA guide sequence rather than the 3'-end (Elbashir *et al.*, 2001, *EMBO J.*, 20, 6877). Other studies have indicated that a 5'-phosphate on the target-complementary strand of a siRNA duplex is required for siRNA activity and that ATP is utilized to maintain the 5'-phosphate moiety on the siRNA (Nykanen *et al.*, 2001, *Cell*, 107, 309); however, siRNA molecules lacking a 5'-phosphate are active when introduced exogenously, suggesting that 5'-phosphorylation of siRNA constructs may occur *in vivo*.

Synthesis of Nucleic acid Molecules

Synthesis of nucleic acids greater than 100 nucleotides in length is difficult using automated methods, and the therapeutic cost of such molecules is prohibitive. In this invention, small nucleic acid motifs ("small" refers to nucleic acid motifs no more than 100 nucleotides in length, preferably no more than 80 nucleotides in length, and most preferably no more than 50 nucleotides in length; e.g., individual siNA oligonucleotide sequences or siNA sequences synthesized in tandem) are preferably used for exogenous

delivery. The simple structure of these molecules increases the ability of the nucleic acid to invade targeted regions of protein and/or RNA structure. Exemplary molecules of the instant invention are chemically synthesized, and others can similarly be synthesized.

Oligonucleotides (*e.g.*, certain modified oligonucleotides or portions of oligonucleotides lacking ribonucleotides) are synthesized using protocols known in the art, for example as described in Caruthers *et al.*, 1992, *Methods in Enzymology* 211, 3-19, Thompson *et al.*, International PCT Publication No. WO 99/54459, Wincott *et al.*, 1995, *Nucleic Acids Res.* 23, 2677-2684, Wincott *et al.*, 1997, *Methods Mol. Bio.*, 74, 59, Brennan *et al.*, 1998, *Biotechnol Bioeng.*, 61, 33-45, and Brennan, U.S. Pat. No. 6,001,311. All of these references are incorporated herein by reference. The synthesis of oligonucleotides makes use of common nucleic acid protecting and coupling groups, such as dimethoxytrityl at the 5'-end, and phosphoramidites at the 3'-end. In a non-limiting example, small scale syntheses are conducted on a 394 Applied Biosystems, Inc. synthesizer using a 0.2 μ mol scale protocol with a 2.5 min coupling step for 2'-O-methylated nucleotides and a 45 sec coupling step for 2'-deoxy nucleotides or 2'-deoxy-2'-fluoro nucleotides. **Table V** outlines the amounts and the contact times of the reagents used in the synthesis cycle. Alternatively, syntheses at the 0.2 μ mol scale can be performed on a 96-well plate synthesizer, such as the instrument produced by Protogene (Palo Alto, CA) with minimal modification to the cycle. A 33-fold excess (60 μ L of 0.11 M = 6.6 μ mol) of 2'-O-methyl phosphoramidite and a 105-fold excess of S-ethyl tetrazole (60 μ L of 0.25 M = 15 μ mol) can be used in each coupling cycle of 2'-O-methyl residues relative to polymer-bound 5'-hydroxyl. A 22-fold excess (40 μ L of 0.11 M = 4.4 μ mol) of deoxy phosphoramidite and a 70-fold excess of S-ethyl tetrazole (40 μ L of 0.25 M = 10 μ mol) can be used in each coupling cycle of deoxy residues relative to polymer-bound 5'-hydroxyl. Average coupling yields on the 394 Applied Biosystems, Inc. synthesizer, determined by colorimetric quantitation of the trityl fractions, are typically 97.5-99%. Other oligonucleotide synthesis reagents for the 394 Applied Biosystems, Inc. synthesizer include the following: detritylation solution is 3% TCA in methylene chloride (ABI); capping is performed with 16% *N*-methyl imidazole in THF (ABI) and 10% acetic anhydride/10% 2,6-lutidine in THF (ABI); and oxidation solution is 16.9 mM I₂, 49 mM pyridine, 9% water in THF (PERSEPTIVE™). Burdick & Jackson Synthesis Grade acetonitrile is used directly from the reagent bottle. S-Ethyltetrazole solution (0.25 M in

acetonitrile) is made up from the solid obtained from American International Chemical, Inc. Alternately, for the introduction of phosphorothioate linkages, Beaucage reagent (3H-1,2-Benzodithiol-3-one 1,1-dioxide, 0.05 M in acetonitrile) is used.

Deprotection of the DNA-based oligonucleotides is performed as follows: the
5 polymer-bound trityl-on oligoribonucleotide is transferred to a 4 mL glass screw top vial and suspended in a solution of 40% aq. methylamine (1 mL) at 65 °C for 10 min. After cooling to -20 °C, the supernatant is removed from the polymer support. The support is washed three times with 1.0 mL of EtOH:MeCN:H₂O/3:1:1, vortexed and the supernatant is then added to the first supernatant. The combined supernatants, containing the
10 oligoribonucleotide, are dried to a white powder.

The method of synthesis used for RNA including certain siNA molecules of the invention follows the procedure as described in Usman *et al.*, 1987, *J. Am. Chem. Soc.*, 109, 7845; Scaringe *et al.*, 1990, *Nucleic Acids Res.*, 18, 5433; and Wincott *et al.*, 1995, *Nucleic Acids Res.* 23, 2677-2684 Wincott *et al.*, 1997, *Methods Mol. Bio.*, 74, 59, and
15 makes use of common nucleic acid protecting and coupling groups, such as dimethoxytrityl at the 5'-end, and phosphoramidites at the 3'-end. In a non-limiting example, small scale syntheses are conducted on a 394 Applied Biosystems, Inc. synthesizer using a 0.2 µmol scale protocol with a 7.5 min coupling step for alkylsilyl protected nucleotides and a 2.5 min coupling step for 2'-O-methylated nucleotides. **Table**
20 **V** outlines the amounts and the contact times of the reagents used in the synthesis cycle. Alternatively, syntheses at the 0.2 µmol scale can be done on a 96-well plate synthesizer, such as the instrument produced by Protogene (Palo Alto, CA) with minimal modification to the cycle. A 33-fold excess (60 µL of 0.11 M = 6.6 µmol) of 2'-O-methyl phosphoramidite and a 75-fold excess of S-ethyl tetrazole (60 µL of 0.25 M = 15 µmol)
25 can be used in each coupling cycle of 2'-O-methyl residues relative to polymer-bound 5'-hydroxyl. A 66-fold excess (120 µL of 0.11 M = 13.2 µmol) of alkylsilyl (ribo) protected phosphoramidite and a 150-fold excess of S-ethyl tetrazole (120 µL of 0.25 M = 30 µmol) can be used in each coupling cycle of ribo residues relative to polymer-bound 5'-hydroxyl. Average coupling yields on the 394 Applied Biosystems, Inc. synthesizer,
30 determined by colorimetric quantitation of the trityl fractions, are typically 97.5-99%. Other oligonucleotide synthesis reagents for the 394 Applied Biosystems, Inc. synthesizer include the following: detritylation solution is 3% TCA in methylene chloride (ABI);

capping is performed with 16% *N*-methyl imidazole in THF (ABI) and 10% acetic anhydride/10% 2,6-lutidine in THF (ABI); oxidation solution is 16.9 mM I₂, 49 mM pyridine, 9% water in THF (PERSEPTIVE™). Burdick & Jackson Synthesis Grade acetonitrile is used directly from the reagent bottle. S-Ethyltetrazole solution (0.25 M in acetonitrile) is made up from the solid obtained from American International Chemical, Inc. Alternately, for the introduction of phosphorothioate linkages, Beaucage reagent (3H-1,2-Benzodithiol-3-one 1,1-dioxide 0.05 M in acetonitrile) is used.

Deprotection of the RNA is performed using either a two-pot or one-pot protocol. For the two-pot protocol, the polymer-bound trityl-on oligoribonucleotide is transferred to a 4 mL glass screw top vial and suspended in a solution of 40% aq. methylamine (1 mL) at 65 °C for 10 min. After cooling to -20 °C, the supernatant is removed from the polymer support. The support is washed three times with 1.0 mL of EtOH:MeCN:H₂O/3:1:1, vortexed and the supernatant is then added to the first supernatant. The combined supernatants, containing the oligoribonucleotide, are dried to a white powder. The base deprotected oligoribonucleotide is resuspended in anhydrous TEA/HF/NMP solution (300 µL of a solution of 1.5 mL *N*-methylpyrrolidinone, 750 µL TEA and 1 mL TEA•3HF to provide a 1.4 M HF concentration) and heated to 65 °C. After 1.5 h, the oligomer is quenched with 1.5 M NH₄HCO₃.

Alternatively, for the one-pot protocol, the polymer-bound trityl-on oligoribonucleotide is transferred to a 4 mL glass screw top vial and suspended in a solution of 33% ethanolic methylamine/DMSO: 1/1 (0.8 mL) at 65 °C for 15 min. The vial is brought to rt. TEA•3HF (0.1 mL) is added and the vial is heated at 65 °C for 15 min. The sample is cooled at -20 °C and then quenched with 1.5 M NH₄HCO₃.

For purification of the trityl-on oligomers, the quenched NH₄HCO₃ solution is loaded onto a C-18 containing cartridge that had been prewashed with acetonitrile followed by 50 mM TEAA. After washing the loaded cartridge with water, the RNA is detritylated with 0.5% TFA for 13 min. The cartridge is then washed again with water, salt exchanged with 1 M NaCl and washed with water again. The oligonucleotide is then eluted with 30% acetonitrile.

The average stepwise coupling yields are typically >98% (Wincott *et al.*, 1995 *Nucleic Acids Res.* 23, 2677-2684). Those of ordinary skill in the art will recognize that the scale of synthesis can be adapted to be larger or smaller than the example described above including but not limited to 96-well format.

5 Alternatively, the nucleic acid molecules of the present invention can be synthesized separately and joined together post-synthetically, for example, by ligation (Moore *et al.*, 1992, *Science* 256, 9923; Draper *et al.*, International PCT publication No. WO 93/23569; Shabarova *et al.*, 1991, *Nucleic Acids Research* 19, 4247; Bellon *et al.*, 1997, *Nucleosides & Nucleotides*, 16, 951; Bellon *et al.*, 1997, *Bioconjugate Chem.* 8,
10 204), or by hybridization following synthesis and/or deprotection.

 The siNA molecules of the invention can also be synthesized via a tandem synthesis methodology as described in Example 1 herein, wherein both siNA strands are synthesized as a single contiguous oligonucleotide fragment or strand separated by a cleavable linker which is subsequently cleaved to provide separate siNA fragments or
15 strands that hybridize and permit purification of the siNA duplex. The linker can be a polynucleotide linker or a non-nucleotide linker. The tandem synthesis of siNA as described herein can be readily adapted to both multiwell/multiplate synthesis platforms such as 96 well or similarly larger multi-well platforms. The tandem synthesis of siNA as described herein can also be readily adapted to large scale synthesis platforms employing
20 batch reactors, synthesis columns and the like.

 A siNA molecule can also be assembled from two distinct nucleic acid strands or fragments wherein one fragment includes the sense region and the second fragment includes the antisense region of the RNA molecule.

 The nucleic acid molecules of the present invention can be modified extensively to
25 enhance stability by modification with nuclease resistant groups, for example, 2'-amino, 2'-C-allyl, 2'-fluoro, 2'-O-methyl, 2'-H (for a review see Usman and Cedergren, 1992, *TIBS* 17, 34; Usman *et al.*, 1994, *Nucleic Acids Symp. Ser.* 31, 163). siNA constructs can be purified by gel electrophoresis using general methods or can be purified by high pressure liquid chromatography (HPLC; see Wincott *et al.*, *supra*, the totality of which is
30 hereby incorporated herein by reference) and re-suspended in water.

In another aspect of the invention, siNA molecules of the invention are expressed from transcription units inserted into DNA or RNA vectors. The recombinant vectors can be DNA plasmids or viral vectors. siNA expressing viral vectors can be constructed based on, but not limited to, adeno-associated virus, retrovirus, adenovirus, or alphavirus. The recombinant vectors capable of expressing the siNA molecules can be delivered as described herein, and persist in target cells. Alternatively, viral vectors can be used that provide for transient expression of siNA molecules.

Optimizing Activity of the nucleic acid molecule of the invention.

Chemically synthesizing nucleic acid molecules with modifications (base, sugar and/or phosphate) can prevent their degradation by serum ribonucleases, which can increase their potency (see *e.g.*, Eckstein *et al.*, International Publication No. WO 92/07065; Perrault *et al.*, 1990 *Nature* 344, 565; Pieken *et al.*, 1991, *Science* 253, 314; Usman and Cedergren, 1992, *Trends in Biochem. Sci.* 17, 334; Usman *et al.*, International Publication No. WO 93/15187; and Rossi *et al.*, International Publication No. WO 91/03162; Sproat, U.S. Pat. No. 5,334,711; Gold *et al.*, U.S. Pat. No. 6,300,074; and Burgin *et al.*, *supra*; all of which are incorporated by reference herein). All of the above references describe various chemical modifications that can be made to the base, phosphate and/or sugar moieties of the nucleic acid molecules described herein. Modifications that enhance their efficacy in cells, and removal of bases from nucleic acid molecules to shorten oligonucleotide synthesis times and reduce chemical requirements are desired.

There are several examples in the art describing sugar, base and phosphate modifications that can be introduced into nucleic acid molecules with significant enhancement in their nuclease stability and efficacy. For example, oligonucleotides are modified to enhance stability and/or enhance biological activity by modification with nuclease resistant groups, for example, 2'-amino, 2'-C-allyl, 2'-fluoro, 2'-O-methyl, 2'-O-allyl, 2'-H, nucleotide base modifications (for a review see Usman and Cedergren, 1992, *TIBS*. 17, 34; Usman *et al.*, 1994, *Nucleic Acids Symp. Ser.* 31, 163; Burgin *et al.*, 1996, *Biochemistry*, 35, 14090). Sugar modification of nucleic acid molecules have been extensively described in the art (see Eckstein *et al.*, International Publication PCT No. WO 92/07065; Perrault *et al.* *Nature*, 1990, 344, 565-568; Pieken *et al.* *Science*, 1991,

253, 314-317; Usman and Cedergren, *Trends in Biochem. Sci.*, 1992, 17, 334-339; Usman *et al.* International Publication PCT No. WO 93/15187; Sproat, U.S. Pat. No. 5,334,711 and Beigelman *et al.*, 1995, *J. Biol. Chem.*, 270, 25702; Beigelman *et al.*, International PCT publication No. WO 97/26270; Beigelman *et al.*, U.S. Pat. No. 5,716,824; Usman *et al.*, U.S. Pat. No. 5,627,053; Woolf *et al.*, International PCT Publication No. WO 98/13526; Thompson *et al.*, USSN 60/082,404 which was filed on April 20, 1998; Karpeisky *et al.*, 1998, *Tetrahedron Lett.*, 39, 1131; Earnshaw and Gait, 1998, *Biopolymers (Nucleic Acid Sciences)*, 48, 39-55; Verma and Eckstein, 1998, *Annu. Rev. Biochem.*, 67, 99-134; and Burlina *et al.*, 1997, *Bioorg. Med. Chem.*, 5, 1999-2010; all of the references are hereby incorporated in their totality by reference herein). Such publications describe general methods and strategies to determine the location of incorporation of sugar, base and/or phosphate modifications and the like into nucleic acid molecules without modulating catalysis, and are incorporated by reference herein. In view of such teachings, similar modifications can be used as described herein to modify the siNA nucleic acid molecules of the instant invention so long as the ability of siNA to promote RNAi in cells is not significantly inhibited.

While chemical modification of oligonucleotide internucleotide linkages with phosphorothioate, phosphorodithioate, and/or 5'-methylphosphonate linkages improves stability, excessive modifications can cause some toxicity or decreased activity. Therefore, when designing nucleic acid molecules, the amount of these internucleotide linkages should be minimized. The reduction in the concentration of these linkages should lower toxicity, resulting in increased efficacy and higher specificity of these molecules.

Short interfering nucleic acid (siNA) molecules having chemical modifications that maintain or enhance activity are provided. Such a nucleic acid is also generally more resistant to nucleases than an unmodified nucleic acid. Accordingly, the *in vitro* and/or *in vivo* activity should not be significantly lowered. In cases in which modulation is the goal, therapeutic nucleic acid molecules delivered exogenously should optimally be stable within cells until translation of the target RNA has been modulated long enough to reduce the levels of the undesirable protein. This period of time varies between hours to days depending upon the disease state. Improvements in the chemical synthesis of RNA and DNA (Wincott *et al.*, 1995, *Nucleic Acids Res.* 23, 2677; Caruthers *et al.*, 1992, *Methods*

in *Enzymology* 211,3-19 (incorporated by reference herein)) have expanded the ability to modify nucleic acid molecules by introducing nucleotide modifications to enhance their nuclease stability, as described above.

In one embodiment, nucleic acid molecules of the invention include one or more
5 (e.g., about 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, or more) G-clamp nucleotides. A G-clamp nucleotide is a modified cytosine analog wherein the modifications confer the ability to hydrogen bond both Watson-Crick and Hoogsteen faces of a complementary guanine within a duplex, see for example Lin and Matteucci, 1998, *J. Am. Chem. Soc.*, 120, 8531-8532. A single G-clamp analog substitution within an oligonucleotide can result in
10 substantially enhanced helical thermal stability and mismatch discrimination when hybridized to complementary oligonucleotides. The inclusion of such nucleotides in nucleic acid molecules of the invention results in both enhanced affinity and specificity to nucleic acid targets, complementary sequences, or template strands. In another embodiment, nucleic acid molecules of the invention include one or more (e.g., about 1,
15 2, 3, 4, 5, 6, 7, 8, 9, 10, or more) LNA "locked nucleic acid" nucleotides such as a 2', 4'-C methylene bicyclo nucleotide (see for example Wengel *et al.*, International PCT Publication No. WO 00/66604 and WO 99/14226).

In another embodiment, the invention features conjugates and/or complexes of siNA molecules of the invention. Such conjugates and/or complexes can be used to
20 facilitate delivery of siNA molecules into a biological system, such as a cell. The conjugates and complexes provided by the instant invention can impart therapeutic activity by transferring therapeutic compounds across cellular membranes, altering the pharmacokinetics, and/or modulating the localization of nucleic acid molecules of the invention. The present invention encompasses the design and synthesis of novel
25 conjugates and complexes for the delivery of molecules, including, but not limited to, small molecules, lipids, phospholipids, nucleosides, nucleotides, nucleic acids, antibodies, toxins, negatively charged polymers and other polymers, for example proteins, peptides, hormones, carbohydrates, polyethylene glycols, or polyamines, across cellular membranes. In general, the transporters described are designed to be used either
30 individually or as part of a multi-component system, with or without degradable linkers. These compounds are expected to improve delivery and/or localization of nucleic acid molecules of the invention into a number of cell types originating from different tissues,

in the presence or absence of serum (see Sullenger and Cech, U.S. Pat. No. 5,854,038). Conjugates of the molecules described herein can be attached to biologically active molecules via linkers that are biodegradable, such as biodegradable nucleic acid linker molecules.

5 The term "biodegradable linker" as used herein, refers to a nucleic acid or non-nucleic acid linker molecule that is designed as a biodegradable linker to connect one molecule to another molecule, for example, a biologically active molecule to a siNA molecule of the invention or the sense and antisense strands of a siNA molecule of the invention. The biodegradable linker is designed such that its stability can be modulated
10 for a particular purpose, such as delivery to a particular tissue or cell type. The stability of a nucleic acid-based biodegradable linker molecule can be modulated by using various chemistries, for example combinations of ribonucleotides, deoxyribonucleotides, and chemically-modified nucleotides, such as 2'-O-methyl, 2'-fluoro, 2'-amino, 2'-O-amino, 2'-C-allyl, 2'-O-allyl, and other 2'-modified or base modified nucleotides. The
15 biodegradable nucleic acid linker molecule can be a dimer, trimer, tetramer or longer nucleic acid molecule, for example, an oligonucleotide of about 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, or 20 nucleotides in length, or can comprise a single nucleotide with a phosphorus-based linkage, for example, a phosphoramidate or phosphodiester linkage. The biodegradable nucleic acid linker molecule can also
20 comprise nucleic acid backbone, nucleic acid sugar, or nucleic acid base modifications.

The term "biodegradable" as used herein, refers to degradation in a biological system, for example enzymatic degradation or chemical degradation.

The term "biologically active molecule" as used herein, refers to compounds or molecules that are capable of eliciting or modifying a biological response in a system.
25 Non-limiting examples of biologically active siNA molecules either alone or in combination with other molecules contemplated by the instant invention include therapeutically active molecules such as antibodies, hormones, antivirals, peptides, proteins, chemotherapeutics, small molecules, vitamins, co-factors, nucleosides, nucleotides, oligonucleotides, enzymatic nucleic acids, antisense nucleic acids, triplex
30 forming oligonucleotides, 2,5-A chimeras, siNA, dsRNA, allozymes, aptamers, decoys and analogs thereof. Biologically active molecules of the invention also include

molecules capable of modulating the pharmacokinetics and/or pharmacodynamics of other biologically active molecules, for example, lipids and polymers such as polyamines, polyamides, polyethylene glycol and other polyethers.

5 The term "phospholipid" as used herein, refers to a hydrophobic molecule comprising at least one phosphorus group. For example, a phospholipid can comprise a phosphorus-containing group and saturated or unsaturated alkyl group, optionally substituted with OH, COOH, oxo, amine, or substituted or unsubstituted aryl groups.

10 Therapeutic nucleic acid molecules (e.g., siNA molecules) delivered exogenously optimally are stable within cells until reverse transcription of the RNA has been modulated long enough to reduce the levels of the RNA transcript. The nucleic acid molecules are resistant to nucleases in order to function as effective intracellular therapeutic agents. Improvements in the chemical synthesis of nucleic acid molecules described in the instant invention and in the art have expanded the ability to modify nucleic acid molecules by introducing nucleotide modifications to enhance their nuclease
15 stability as described above.

In yet another embodiment, siNA molecules having chemical modifications that maintain or enhance enzymatic activity of proteins involved in RNAi are provided. Such nucleic acids are also generally more resistant to nucleases than unmodified nucleic acids. Thus, *in vitro* and/or *in vivo* the activity should not be significantly lowered.

20 Use of the nucleic acid-based molecules of the invention will lead to better treatment of the disease progression by affording the possibility of combination therapies (e.g., multiple siNA molecules targeted to different genes; nucleic acid molecules coupled with known small molecule modulators; or intermittent treatment with combinations of molecules, including different motifs and/or other chemical or biological molecules). The
25 treatment of subjects with siNA molecules can also include combinations of different types of nucleic acid molecules, such as enzymatic nucleic acid molecules (ribozymes), allozymes, antisense, 2,5-A oligoadenylate, decoys, and aptamers.

In another aspect a siNA molecule of the invention comprises one or more 5' and/or a 3'- cap structure, for example on only the sense siNA strand, the antisense siNA strand,
30 or both siNA strands.

By "cap structure" is meant chemical modifications, which have been incorporated at either terminus of the oligonucleotide (see, for example, Adamic *et al.*, U.S. Pat. No. 5,998,203, incorporated by reference herein). These terminal modifications protect the nucleic acid molecule from exonuclease degradation, and may help in delivery and/or localization within a cell. The cap may be present at the 5'-terminus (5'-cap) or at the 3'-terminal (3'-cap) or may be present on both termini. In non-limiting examples the 5'-cap is selected from the group consisting of glyceryl, inverted deoxy abasic residue (moiety); 4',5'-methylene nucleotide; 1-(beta-D-erythrofuransyl) nucleotide, 4'-thio nucleotide; carbocyclic nucleotide; 1,5-anhydrohexitol nucleotide; L-nucleotides; alpha-nucleotides; modified base nucleotide; phosphorodithioate linkage; *threo*-pentofuransyl nucleotide; acyclic 3',4'-seco nucleotide; acyclic 3,4-dihydroxybutyl nucleotide; acyclic 3,5-dihydroxypentyl nucleotide, 3'-3'-inverted nucleotide moiety; 3'-3'-inverted abasic moiety; 3'-2'-inverted nucleotide moiety; 3'-2'-inverted abasic moiety; 1,4-butanediol phosphate; 3'-phosphoramidate; hexylphosphate; aminohexyl phosphate; 3'-phosphate; 3'-phosphorothioate; phosphorodithioate; or bridging or non-bridging methylphosphonate moiety.

In non-limiting examples, the 3'-cap is selected from the group consisting of glyceryl, inverted deoxy abasic residue (moiety), 4',5'-methylene nucleotide; 1-(beta-D-erythrofuransyl) nucleotide; 4'-thio nucleotide, carbocyclic nucleotide; 5'-amino-alkyl phosphate; 1,3-diamino-2-propyl phosphate; 3-aminopropyl phosphate; 6-aminohexyl phosphate; 1,2-aminododecyl phosphate; hydroxypropyl phosphate; 1,5-anhydrohexitol nucleotide; L-nucleotide; alpha-nucleotide; modified base nucleotide; phosphorodithioate; *threo*-pentofuransyl nucleotide; acyclic 3',4'-seco nucleotide; 3,4-dihydroxybutyl nucleotide; 3,5-dihydroxypentyl nucleotide, 5'-5'-inverted nucleotide moiety; 5'-5'-inverted abasic moiety; 5'-phosphoramidate; 5'-phosphorothioate; 1,4-butanediol phosphate; 5'-amino; bridging and/or non-bridging 5'-phosphoramidate, phosphorothioate and/or phosphorodithioate, bridging or non bridging methylphosphonate and 5'-mercapto moieties (for more details see Beaucage and Iyer, 1993, *Tetrahedron* 49, 1925; incorporated by reference herein).

By the term "non-nucleotide" is meant any group or compound which can be incorporated into a nucleic acid chain in the place of one or more nucleotide units, including either sugar and/or phosphate substitutions, and allows the remaining bases to

exhibit their enzymatic activity. The group or compound is abasic in that it does not contain a commonly recognized nucleotide base, such as adenosine, guanine, cytosine, uracil or thymine and therefore lacks a base at the 1'-position.

An "alkyl" group refers to a saturated aliphatic hydrocarbon, including straight-chain, branched-chain, and cyclic alkyl groups. Preferably, the alkyl group has 1 to 12 carbons. More preferably, it is a lower alkyl of from 1 to 7 carbons, more preferably 1 to 4 carbons. The alkyl group can be substituted or unsubstituted. When substituted the substituted group(s) is preferably, hydroxyl, cyano, alkoxy, =O, =S, NO₂ or N(CH₃)₂, amino, or SH. The term also includes alkenyl groups that are unsaturated hydrocarbon groups containing at least one carbon-carbon double bond, including straight-chain, branched-chain, and cyclic groups. Preferably, the alkenyl group has 1 to 12 carbons. More preferably, it is a lower alkenyl of from 1 to 7 carbons, more preferably 1 to 4 carbons. The alkenyl group may be substituted or unsubstituted. When substituted the substituted group(s) is preferably, hydroxyl, cyano, alkoxy, =O, =S, NO₂, halogen, N(CH₃)₂, amino, or SH. The term "alkyl" also includes alkynyl groups that have an unsaturated hydrocarbon group containing at least one carbon-carbon triple bond, including straight-chain, branched-chain, and cyclic groups. Preferably, the alkynyl group has 1 to 12 carbons. More preferably, it is a lower alkynyl of from 1 to 7 carbons, more preferably 1 to 4 carbons. The alkynyl group may be substituted or unsubstituted. When substituted the substituted group(s) is preferably, hydroxyl, cyano, alkoxy, =O, =S, NO₂ or N(CH₃)₂, amino or SH.

Such alkyl groups can also include aryl, alkylaryl, carbocyclic aryl, heterocyclic aryl, amide and ester groups. An "aryl" group refers to an aromatic group that has at least one ring having a conjugated pi electron system and includes carbocyclic aryl, heterocyclic aryl and biaryl groups, all of which may be optionally substituted. The preferred substituent(s) of aryl groups are halogen, trihalomethyl, hydroxyl, SH, OH, cyano, alkoxy, alkyl, alkenyl, alkynyl, and amino groups. An "alkylaryl" group refers to an alkyl group (as described above) covalently joined to an aryl group (as described above). Carbocyclic aryl groups are groups wherein the ring atoms on the aromatic ring are all carbon atoms. The carbon atoms are optionally substituted. Heterocyclic aryl groups are groups having from 1 to 3 heteroatoms as ring atoms in the aromatic ring and

the remainder of the ring atoms are carbon atoms. Suitable heteroatoms include oxygen, sulfur, and nitrogen, and include furanyl, thienyl, pyridyl, pyrrolyl, N-lower alkyl pyrrolo, pyrimidyl, pyrazinyl, imidazolyl and the like, all optionally substituted. An "amide" refers to an -C(O)-NH-R, where R is either alkyl, aryl, alkylaryl or hydrogen. An "ester" refers to an -C(O)-OR', where R is either alkyl, aryl, alkylaryl or hydrogen.

By "nucleotide" as used herein is as recognized in the art to include natural bases (standard), and modified bases well known in the art. Such bases are generally located at the 1' position of a nucleotide sugar moiety. Nucleotides generally comprise a base, sugar and a phosphate group. The nucleotides can be unmodified or modified at the sugar, phosphate and/or base moiety, (also referred to interchangeably as nucleotide analogs, modified nucleotides, non-natural nucleotides, non-standard nucleotides and other; see, for example, Usman and McSwiggen, *supra*; Eckstein *et al.*, International PCT Publication No. WO 92/07065; Usman *et al.*, International PCT Publication No. WO 93/15187; Uhlman & Peyman, *supra*, all are hereby incorporated by reference herein). There are several examples of modified nucleic acid bases known in the art as summarized by Limbach *et al.*, 1994, *Nucleic Acids Res.* 22, 2183. Some of the non-limiting examples of base modifications that can be introduced into nucleic acid molecules include, inosine, purine, pyridin-4-one, pyridin-2-one, phenyl, pseudouracil, 2, 4, 6-trimethoxy benzene, 3-methyl uracil, dihydrouridine, naphthyl, aminophenyl, 5-alkylcytidines (*e.g.*, 5-methylcytidine), 5-alkyluridines (*e.g.*, ribothymidine), 5-halouridine (*e.g.*, 5-bromouridine) or 6-azapyrimidines or 6-alkylpyrimidines (*e.g.* 6-methyluridine), propyne, and others (Burgin *et al.*, 1996, *Biochemistry*, 35, 14090; Uhlman & Peyman, *supra*). By "modified bases" in this aspect is meant nucleotide bases other than adenine, guanine, cytosine and uracil at 1' position or their equivalents.

In one embodiment, the invention features modified siNA molecules, with phosphate backbone modifications comprising one or more phosphorothioate, phosphorodithioate, methylphosphonate, phosphotriester, morpholino, amidate carbamate, carboxymethyl, acetamidate, polyamide, sulfonate, sulfonamide, sulfamate, formacetal, thioformacetal, and/or alkylsilyl, substitutions. For a review of oligonucleotide backbone modifications, see Hunziker and Leumann, 1995, *Nucleic Acid Analogues: Synthesis and Properties*, in *Modern Synthetic Methods*, VCH, 331-417, and

Mesmaeker *et al.*, 1994, *Novel Backbone Replacements for Oligonucleotides*, in *Carbohydrate Modifications in Antisense Research*, ACS, 24-39.

By "abasic" is meant sugar moieties lacking a base or having other chemical groups in place of a base at the 1' position, see for example Adamic *et al.*, U.S. Pat. No. 5,998,203.

By "unmodified nucleoside" is meant one of the bases adenine, cytosine, guanine, thymine, or uracil joined to the 1' carbon of β -D-ribo-furanose.

By "modified nucleoside" is meant any nucleotide base which contains a modification in the chemical structure of an unmodified nucleotide base, sugar and/or phosphate. Non-limiting examples of modified nucleotides are shown by Formulae I-VII and/or other modifications described herein.

In connection with 2'-modified nucleotides as described for the present invention, by "amino" is meant 2'-NH₂ or 2'-O- NH₂, which can be modified or unmodified. Such modified groups are described, for example, in Eckstein *et al.*, U.S. Pat. No. 5,672,695 and Matulic-Adamic *et al.*, U.S. Pat. No. 6,248,878, which are both incorporated by reference in their entireties.

Various modifications to nucleic acid siNA structure can be made to enhance the utility of these molecules. Such modifications will enhance shelf-life, half-life *in vitro*, stability, and ease of introduction of such oligonucleotides to the target site, *e.g.*, to enhance penetration of cellular membranes, and confer the ability to recognize and bind to targeted cells.

Administration of Nucleic Acid Molecules

A siNA molecule of the invention can be adapted for use to treat for example cancer, restenosis, polycystic kidney disease and other indications that can respond to the level of PDGF and/or PDGFr in a cell or tissue, alone or in combination with other therapies. For example, a siNA molecule can comprise a delivery vehicle, including liposomes, for administration to a subject, carriers and diluents and their salts, and/or can be present in pharmaceutically acceptable formulations. Methods for the delivery of nucleic acid molecules are described in Akhtar *et al.*, 1992, *Trends Cell Bio.*, 2, 139;

Delivery Strategies for Antisense Oligonucleotide Therapeutics, ed. Akhtar, 1995, Maurer *et al.*, 1999, *Mol. Membr. Biol.*, 16, 129-140; Hofland and Huang, 1999, *Handb. Exp. Pharmacol.*, 137, 165-192; and Lee *et al.*, 2000, *ACS Symp. Ser.*, 752, 184-192, all of which are incorporated herein by reference. Beigelman *et al.*, U.S. Pat. No. 6,395,713 and Sullivan *et al.*, PCT WO 94/02595 further describe the general methods for delivery of nucleic acid molecules. These protocols can be utilized for the delivery of virtually any nucleic acid molecule. Nucleic acid molecules can be administered to cells by a variety of methods known to those of skill in the art, including, but not restricted to, encapsulation in liposomes, by iontophoresis, or by incorporation into other vehicles, such as hydrogels, cyclodextrins (see for example Gonzalez *et al.*, 1999, *Bioconjugate Chem.*, 10, 1068-1074), biodegradable nanocapsules, and bioadhesive microspheres, or by proteinaceous vectors (O'Hare and Normand, International PCT Publication No. WO 00/53722). Alternatively, the nucleic acid/vehicle combination is locally delivered by direct injection or by use of an infusion pump. Direct injection of the nucleic acid molecules of the invention, whether subcutaneous, intramuscular, or intradermal, can take place using standard needle and syringe methodologies, or by needle-free technologies such as those described in Conry *et al.*, 1999, *Clin. Cancer Res.*, 5, 2330-2337 and Barry *et al.*, International PCT Publication No. WO 99/31262. The molecules of the instant invention can be used as pharmaceutical agents. Pharmaceutical agents prevent, modulate the occurrence, or treat (alleviate a symptom to some extent, preferably all of the symptoms) of a disease state in a subject.

Thus, the invention features a pharmaceutical composition comprising one or more nucleic acid(s) of the invention in an acceptable carrier, such as a stabilizer, buffer, and the like. The polynucleotides of the invention can be administered (*e.g.*, RNA, DNA or protein) and introduced into a subject by any standard means, with or without stabilizers, buffers, and the like, to form a pharmaceutical composition. When it is desired to use a liposome delivery mechanism, standard protocols for formation of liposomes can be followed. The compositions of the present invention can also be formulated and used as tablets, capsules or elixirs for oral administration, suppositories for rectal administration, sterile solutions, suspensions for injectable administration, and the other compositions known in the art.

The present invention also includes pharmaceutically acceptable formulations of the compounds described. These formulations include salts of the above compounds, *e.g.*, acid addition salts, for example, salts of hydrochloric, hydrobromic, acetic acid, and benzene sulfonic acid.

5 A pharmacological composition or formulation refers to a composition or formulation in a form suitable for administration, *e.g.*, systemic administration, into a cell or subject, including for example a human. Suitable forms, in part, depend upon the use or the route of entry, for example oral, transdermal, or by injection. Such forms should not prevent the composition or formulation from reaching a target cell (*i.e.*, a cell to
10 which the negatively charged nucleic acid is desirable for delivery). For example, pharmacological compositions injected into the blood stream should be soluble. Other factors are known in the art, and include considerations such as toxicity and forms that prevent the composition or formulation from exerting its effect.

 By "systemic administration" is meant *in vivo* systemic absorption or accumulation
15 of drugs in the blood stream followed by distribution throughout the entire body. Administration routes that lead to systemic absorption include, without limitation: intravenous, subcutaneous, intraperitoneal, inhalation, oral, intrapulmonary and intramuscular. Each of these administration routes exposes the siNA molecules of the invention to an accessible diseased tissue. The rate of entry of a drug into the circulation
20 has been shown to be a function of molecular weight or size. The use of a liposome or other drug carrier comprising the compounds of the instant invention can potentially localize the drug, for example, in certain tissue types, such as the tissues of the reticular endothelial system (RES). A liposome formulation that can facilitate the association of drug with the surface of cells, such as, lymphocytes and macrophages is also useful. This
25 approach can provide enhanced delivery of the drug to target cells by taking advantage of the specificity of macrophage and lymphocyte immune recognition of abnormal cells, such as cells producing excess PDGF and/or PDGFr.

 By "pharmaceutically acceptable formulation" is meant, a composition or formulation that allows for the effective distribution of the nucleic acid molecules of the
30 instant invention in the physical location most suitable for their desired activity. Non-limiting examples of agents suitable for formulation with the nucleic acid molecules of

the instant invention include: P-glycoprotein inhibitors (such as Pluronic P85), which can enhance entry of drugs into the CNS (Joliet-Riant and Tillement, 1999, *Fundam. Clin. Pharmacol.*, 13, 16-26); biodegradable polymers, such as poly (DL-lactide-coglycolide) microspheres for sustained release delivery after intracerebral implantation (Emerich, DF
5 *et al.*, 1999, *Cell Transplant*, 8, 47-58) (Alkermes, Inc. Cambridge, MA); and loaded nanoparticles, such as those made of polybutylcyanoacrylate, which can deliver drugs across the blood brain barrier and can alter neuronal uptake mechanisms (*Prog Neuropsychopharmacol Biol Psychiatry*, 23, 941-949, 1999). Other non-limiting examples of delivery strategies for the nucleic acid molecules of the instant invention
10 include material described in Boado *et al.*, 1998, *J. Pharm. Sci.*, 87, 1308-1315; Tyler *et al.*, 1999, *FEBS Lett.*, 421, 280-284; Pardridge *et al.*, 1995, *PNAS USA.*, 92, 5592-5596; Boado, 1995, *Adv. Drug Delivery Rev.*, 15, 73-107; Aldrian-Herrada *et al.*, 1998, *Nucleic Acids Res.*, 26, 4910-4916; and Tyler *et al.*, 1999, *PNAS USA.*, 96, 7053-7058.

The invention also features the use of the composition comprising surface-modified
15 liposomes containing poly (ethylene glycol) lipids (PEG-modified, or long-circulating liposomes or stealth liposomes). These formulations offer a method for increasing the accumulation of drugs in target tissues. This class of drug carriers resists opsonization and elimination by the mononuclear phagocytic system (MPS or RES), thereby enabling longer blood circulation times and enhanced tissue exposure for the encapsulated drug
20 (Lasic *et al. Chem. Rev.* 1995, 95, 2601-2627; Ishiwata *et al., Chem. Pharm. Bull.* 1995, 43, 1005-1011). Such liposomes have been shown to accumulate selectively in tumors, presumably by extravasation and capture in the neovascularized target tissues (Lasic *et al., Science* 1995, 267, 1275-1276; Oku *et al., Biochim. Biophys. Acta*, 1238, 86-90). The long-circulating liposomes enhance the pharmacokinetics and
25 pharmacodynamics of DNA and RNA, particularly compared to conventional cationic liposomes which are known to accumulate in tissues of the MPS (Liu *et al., J. Biol. Chem.* 1995, 42, 24864-24870; Choi *et al.*, International PCT Publication No. WO 96/10391; Ansell *et al.*, International PCT Publication No. WO 96/10390; Holland *et al.*, International PCT Publication No. WO 96/10392). Long-circulating liposomes are also
30 likely to protect drugs from nuclease degradation to a greater extent compared to cationic liposomes, based on their ability to avoid accumulation in metabolically aggressive MPS tissues such as the liver and spleen.

The present invention also includes compositions prepared for storage or administration that include a pharmaceutically effective amount of the desired compounds in a pharmaceutically acceptable carrier or diluent. Acceptable carriers or diluents for therapeutic use are well known in the pharmaceutical art, and are described, for example, in *Remington's Pharmaceutical Sciences*, Mack Publishing Co. (A.R. Gennaro edit. 1985), hereby incorporated by reference herein. For example, preservatives, stabilizers, dyes and flavoring agents can be provided. These include sodium benzoate, sorbic acid and esters of *p*-hydroxybenzoic acid. In addition, antioxidants and suspending agents can be used.

A pharmaceutically effective dose is that dose required to prevent, inhibit the occurrence, or treat (alleviate a symptom to some extent, preferably all of the symptoms) of a disease state. The pharmaceutically effective dose depends on the type of disease, the composition used, the route of administration, the type of mammal being treated, the physical characteristics of the specific mammal under consideration, concurrent medication, and other factors that those skilled in the medical arts will recognize. Generally, an amount between 0.1 mg/kg and 100 mg/kg body weight/day of active ingredients is administered dependent upon potency of the negatively charged polymer.

The nucleic acid molecules of the invention and formulations thereof can be administered orally, topically, parenterally, by inhalation or spray, or rectally in dosage unit formulations containing conventional non-toxic pharmaceutically acceptable carriers, adjuvants and/or vehicles. The term parenteral as used herein includes percutaneous, subcutaneous, intravascular (*e.g.*, intravenous), intramuscular, or intrathecal injection or infusion techniques and the like. In addition, there is provided a pharmaceutical formulation comprising a nucleic acid molecule of the invention and a pharmaceutically acceptable carrier. One or more nucleic acid molecules of the invention can be present in association with one or more non-toxic pharmaceutically acceptable carriers and/or diluents and/or adjuvants, and if desired other active ingredients. The pharmaceutical compositions containing nucleic acid molecules of the invention can be in a form suitable for oral use, for example, as tablets, troches, lozenges, aqueous or oily suspensions, dispersible powders or granules, emulsion, hard or soft capsules, or syrups or elixirs.

Compositions intended for oral use can be prepared according to any method known to the art for the manufacture of pharmaceutical compositions and such compositions can contain one or more such sweetening agents, flavoring agents, coloring agents or preservative agents in order to provide pharmaceutically elegant and palatable preparations. Tablets contain the active ingredient in admixture with non-toxic pharmaceutically acceptable excipients that are suitable for the manufacture of tablets. These excipients can be, for example, inert diluents; such as calcium carbonate, sodium carbonate, lactose, calcium phosphate or sodium phosphate; granulating and disintegrating agents, for example, corn starch, or alginic acid; binding agents, for example starch, gelatin or acacia; and lubricating agents, for example magnesium stearate, stearic acid or talc. The tablets can be uncoated or they can be coated by known techniques. In some cases such coatings can be prepared by known techniques to delay disintegration and absorption in the gastrointestinal tract and thereby provide a sustained action over a longer period. For example, a time delay material such as glyceryl monostearate or glyceryl distearate can be employed.

Formulations for oral use can also be presented as hard gelatin capsules wherein the active ingredient is mixed with an inert solid diluent, for example, calcium carbonate, calcium phosphate or kaolin, or as soft gelatin capsules wherein the active ingredient is mixed with water or an oil medium, for example peanut oil, liquid paraffin or olive oil.

Aqueous suspensions contain the active materials in a mixture with excipients suitable for the manufacture of aqueous suspensions. Such excipients are suspending agents, for example sodium carboxymethylcellulose, methylcellulose, hydropropylmethylcellulose, sodium alginate, polyvinylpyrrolidone, gum tragacanth and gum acacia; dispersing or wetting agents can be a naturally-occurring phosphatide, for example, lecithin, or condensation products of an alkylene oxide with fatty acids, for example polyoxyethylene stearate, or condensation products of ethylene oxide with long chain aliphatic alcohols, for example heptadecaethyleneoxycetanol, or condensation products of ethylene oxide with partial esters derived from fatty acids and a hexitol such as polyoxyethylene sorbitol monooleate, or condensation products of ethylene oxide with partial esters derived from fatty acids and hexitol anhydrides, for example polyethylene sorbitan monooleate. The aqueous suspensions can also contain one or more preservatives, for example ethyl, or n-propyl p-hydroxybenzoate, one or more coloring

agents, one or more flavoring agents, and one or more sweetening agents, such as sucrose or saccharin.

Oily suspensions can be formulated by suspending the active ingredients in a vegetable oil, for example arachis oil, olive oil, sesame oil or coconut oil, or in a mineral oil such as liquid paraffin. The oily suspensions can contain a thickening agent, for example beeswax, hard paraffin or cetyl alcohol. Sweetening agents and flavoring agents can be added to provide palatable oral preparations. These compositions can be preserved by the addition of an anti-oxidant such as ascorbic acid

Dispersible powders and granules suitable for preparation of an aqueous suspension by the addition of water provide the active ingredient in admixture with a dispersing or wetting agent, suspending agent and one or more preservatives. Suitable dispersing or wetting agents or suspending agents are exemplified by those already mentioned above. Additional excipients, for example sweetening, flavoring and coloring agents, can also be present.

Pharmaceutical compositions of the invention can also be in the form of oil-in-water emulsions. The oily phase can be a vegetable oil or a mineral oil or mixtures of these. Suitable emulsifying agents can be naturally-occurring gums, for example gum acacia or gum tragacanth, naturally-occurring phosphatides, for example soy bean, lecithin, and esters or partial esters derived from fatty acids and hexitol, anhydrides, for example sorbitan monooleate, and condensation products of the said partial esters with ethylene oxide, for example polyoxyethylene sorbitan monooleate. The emulsions can also contain sweetening and flavoring agents.

Syrups and elixirs can be formulated with sweetening agents, for example glycerol, propylene glycol, sorbitol, glucose or sucrose. Such formulations can also contain a demulcent, a preservative and flavoring and coloring agents. The pharmaceutical compositions can be in the form of a sterile injectable aqueous or oleaginous suspension. This suspension can be formulated according to the known art using those suitable dispersing or wetting agents and suspending agents that have been mentioned above. The sterile injectable preparation can also be a sterile injectable solution or suspension in a non-toxic parentally acceptable diluent or solvent, for example as a solution in 1,3-butanediol. Among the acceptable vehicles and solvents that can be employed are water,

Ringer's solution and isotonic sodium chloride solution. In addition, sterile, fixed oils are conventionally employed as a solvent or suspending medium. For this purpose, any bland fixed oil can be employed including synthetic mono-or diglycerides. In addition, fatty acids such as oleic acid find use in the preparation of injectables.

5 The nucleic acid molecules of the invention can also be administered in the form of suppositories, *e.g.*, for rectal administration of the drug. These compositions can be prepared by mixing the drug with a suitable non-irritating excipient that is solid at ordinary temperatures but liquid at the rectal temperature and will therefore melt in the rectum to release the drug. Such materials include cocoa butter and polyethylene glycols.

10 Nucleic acid molecules of the invention can be administered parenterally in a sterile medium. The drug, depending on the vehicle and concentration used, can either be suspended or dissolved in the vehicle. Advantageously, adjuvants such as local anesthetics, preservatives and buffering agents can be dissolved in the vehicle.

15 Dosage levels of the order of from about 0.1 mg to about 140 mg per kilogram of body weight per day are useful in the treatment of the above-indicated conditions (about 0.5 mg to about 7 g per subject per day). The amount of active ingredient that can be combined with the carrier materials to produce a single dosage form varies depending upon the host treated and the particular mode of administration. Dosage unit forms generally contain between from about 1 mg to about 500 mg of an active ingredient.

20 It is understood that the specific dose level for any particular subject depends upon a variety of factors including the activity of the specific compound employed, the age, body weight, general health, sex, diet, time of administration, route of administration, and rate of excretion, drug combination and the severity of the particular disease undergoing therapy.

25 For administration to non-human animals, the composition can also be added to the animal feed or drinking water. It can be convenient to formulate the animal feed and drinking water compositions so that the animal takes in a therapeutically appropriate quantity of the composition along with its diet. It can also be convenient to present the composition as a premix for addition to the feed or drinking water.

The nucleic acid molecules of the present invention can also be administered to a subject in combination with other therapeutic compounds to increase the overall therapeutic effect. The use of multiple compounds to treat an indication can increase the beneficial effects while reducing the presence of side effects.

5 In one embodiment, the invention comprises compositions suitable for administering nucleic acid molecules of the invention to specific cell types. For example, the asialoglycoprotein receptor (ASGPr) (Wu and Wu, 1987, *J. Biol. Chem.* 262, 4429-4432) is unique to hepatocytes and binds branched galactose-terminal glycoproteins, such as asialoorosomucoid (ASOR). In another example, the folate receptor is overexpressed
10 in many cancer cells. Binding of such glycoproteins, synthetic glycoconjugates, or folates to the receptor takes place with an affinity that strongly depends on the degree of branching of the oligosaccharide chain, for example, triantennary structures are bound with greater affinity than biantennary or monoantennary chains (Baenziger and Fiete, 1980, *Cell*, 22, 611-620; Connolly *et al.*, 1982, *J. Biol. Chem.*, 257, 939-945). Lee and Lee, 1987, *Glycoconjugate J.*, 4, 317-328, obtained this high specificity through the use of N-acetyl-D-galactosamine as the carbohydrate moiety, which has higher affinity for the receptor, compared to galactose. This "clustering effect" has also been described for the binding and uptake of mannosyl-terminating glycoproteins or glycoconjugates (Ponpipom *et al.*, 1981, *J. Med. Chem.*, 24, 1388-1395). The use of galactose, galactosamine, or folate
15 based conjugates to transport exogenous compounds across cell membranes can provide a targeted delivery approach to, for example, the treatment of liver disease, cancers of the liver, or other cancers. The use of bioconjugates can also provide a reduction in the required dose of therapeutic compounds required for treatment. Furthermore, therapeutic bioavailability, pharmacodynamics, and pharmacokinetic parameters can be modulated
20 through the use of nucleic acid bioconjugates of the invention. Non-limiting examples of such bioconjugates are described in Vargeese *et al.*, USSN 60/311,865, filed August 13, 2001; and Matulic-Adamic *et al.*, USSN 60/362,016, filed March 6, 2002.

Alternatively, certain siNA molecules of the instant invention can be expressed within cells from eukaryotic promoters (e.g., Izant and Weintraub, 1985, *Science*, 229, 345; McGarry and Lindquist, 1986, *Proc. Natl. Acad. Sci.*, USA 83, 399; Scanlon *et al.*, 1991, *Proc. Natl. Acad. Sci. USA*, 88, 10591-5; Kashani-Sabet *et al.*, 1992, *Antisense Res. Dev.*, 2, 3-15; Dropulic *et al.*, 1992, *J. Virol.*, 66, 1432-41; Weerasinghe *et al.*, 1991, *J.*
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Virol., 65, 5531-4; Ojwang *et al.*, 1992, *Proc. Natl. Acad. Sci. USA*, 89, 10802-6; Chen *et al.*, 1992, *Nucleic Acids Res.*, 20, 4581-9; Sarver *et al.*, 1990 *Science*, 247, 1222-1225; Thompson *et al.*, 1995, *Nucleic Acids Res.*, 23, 2259; Good *et al.*, 1997, *Gene Therapy*, 4, 45. Those skilled in the art realize that any nucleic acid can be expressed in eukaryotic
5 cells from the appropriate DNA/RNA vector. The activity of such nucleic acids can be augmented by their release from the primary transcript by a enzymatic nucleic acid (Draper *et al.*, PCT WO 93/23569, and Sullivan *et al.*, PCT WO 94/02595; Ohkawa *et al.*, 1992, *Nucleic Acids Symp. Ser.*, 27, 15-6; Taira *et al.*, 1991, *Nucleic Acids Res.*, 19, 5125-30; Ventura *et al.*, 1993, *Nucleic Acids Res.*, 21, 3249-55; Chowrira *et al.*, 1994, *J. Biol.*
10 *Chem.*, 269, 25856.

In another aspect of the invention, RNA molecules of the present invention can be expressed from transcription units (see for example Couture *et al.*, 1996, *TIG.*, 12, 510) inserted into DNA or RNA vectors. The recombinant vectors can be DNA plasmids or viral vectors. siNA expressing viral vectors can be constructed based on, but not limited
15 to, adeno-associated virus, retrovirus, adenovirus, or alphavirus. In another embodiment, pol III based constructs are used to express nucleic acid molecules of the invention (see for example Thompson, U.S. Pats. Nos. 5,902,880 and 6,146,886). The recombinant vectors capable of expressing the siNA molecules can be delivered as described above, and persist in target cells. Alternatively, viral vectors can be used that provide for
20 transient expression of nucleic acid molecules. Such vectors can be repeatedly administered as necessary. Once expressed, the siNA molecule interacts with the target mRNA and generates an RNAi response. Delivery of siNA molecule expressing vectors can be systemic, such as by intravenous or intra-muscular administration, by administration to target cells ex-planted from a subject followed by reintroduction into the
25 subject, or by any other means that would allow for introduction into the desired target cell (for a review see Couture *et al.*, 1996, *TIG.*, 12, 510).

In one aspect the invention features an expression vector comprising a nucleic acid sequence encoding at least one siNA molecule of the instant invention. The expression vector can encode one or both strands of a siNA duplex, or a single self-complementary
30 strand that self hybridizes into a siNA duplex. The nucleic acid sequences encoding the siNA molecules of the instant invention can be operably linked in a manner that allows expression of the siNA molecule (see for example Paul *et al.*, 2002, *Nature*

Biotechnology, 19, 505; Miyagishi and Taira, 2002, *Nature Biotechnology*, 19, 497; Lee *et al.*, 2002, *Nature Biotechnology*, 19, 500; and Novina *et al.*, 2002, *Nature Medicine*, advance online publication doi:10.1038/nm725).

In another aspect, the invention features an expression vector comprising: a) a
5 transcription initiation region (*e.g.*, eukaryotic pol I, II or III initiation region); b) a
transcription termination region (*e.g.*, eukaryotic pol I, II or III termination region); and c)
a nucleic acid sequence encoding at least one of the siNA molecules of the instant
invention; wherein said sequence is operably linked to said initiation region and said
termination region, in a manner that allows expression and/or delivery of the siNA
10 molecule. The vector can optionally include an open reading frame (ORF) for a protein
operably linked on the 5' side or the 3'-side of the sequence encoding the siNA of the
invention; and/or an intron (intervening sequences).

Transcription of the siNA molecule sequences can be driven from a promoter for
eukaryotic RNA polymerase I (pol I), RNA polymerase II (pol II), or RNA polymerase III
15 (pol III). Transcripts from pol II or pol III promoters are expressed at high levels in all
cells; the levels of a given pol II promoter in a given cell type depends on the nature of
the gene regulatory sequences (enhancers, silencers, etc.) present nearby. Prokaryotic
RNA polymerase promoters are also used, providing that the prokaryotic RNA
polymerase enzyme is expressed in the appropriate cells (Elroy-Stein and Moss, 1990,
20 *Proc. Natl. Acad. Sci. U S A*, 87, 6743-7; Gao and Huang 1993, *Nucleic Acids Res.*, 21,
2867-72; Lieber *et al.*, 1993, *Methods Enzymol.*, 217, 47-66; Zhou *et al.*, 1990, *Mol.*
Cell. Biol., 10, 4529-37). Several investigators have demonstrated that nucleic acid
molecules expressed from such promoters can function in mammalian cells (*e.g.* Kashani-
Sabet *et al.*, 1992, *Antisense Res. Dev.*, 2, 3-15; Ojwang *et al.*, 1992, *Proc. Natl. Acad.*
25 *Sci. U S A*, 89, 10802-6; Chen *et al.*, 1992, *Nucleic Acids Res.*, 20, 4581-9; Yu *et al.*,
1993, *Proc. Natl. Acad. Sci. U S A*, 90, 6340-4; L'Huillier *et al.*, 1992, *EMBO J.*, 11,
4411-8; Lisziewicz *et al.*, 1993, *Proc. Natl. Acad. Sci. U. S. A*, 90, 8000-4; Thompson *et*
al., 1995, *Nucleic Acids Res.*, 23, 2259; Sullenger & Cech, 1993, *Science*, 262, 1566).
More specifically, transcription units such as the ones derived from genes encoding U6
30 small nuclear (snRNA), transfer RNA (tRNA) and adenovirus VA RNA are useful in
generating high concentrations of desired RNA molecules such as siNA in cells
(Thompson *et al.*, *supra*; Couture and Stinchcomb, 1996, *supra*; Noonberg *et al.*, 1994,

Nucleic Acid Res., 22, 2830; Noonberg *et al.*, U.S. Pat. No. 5,624,803; Good *et al.*, 1997, *Gene Ther.*, 4, 45; Beigelman *et al.*, International PCT Publication No. WO 96/18736. The above siNA transcription units can be incorporated into a variety of vectors for introduction into mammalian cells, including but not restricted to, plasmid DNA vectors, viral DNA vectors (such as adenovirus or adeno-associated virus vectors), or viral RNA vectors (such as retroviral or alphavirus vectors) (for a review see Couture and Stinchcomb, 1996, *supra*).

In another aspect the invention features an expression vector comprising a nucleic acid sequence encoding at least one of the siNA molecules of the invention in a manner that allows expression of that siNA molecule. The expression vector comprises in one embodiment; a) a transcription initiation region; b) a transcription termination region; and c) a nucleic acid sequence encoding at least one strand of the siNA molecule, wherein the sequence is operably linked to the initiation region and the termination region in a manner that allows expression and/or delivery of the siNA molecule.

In another embodiment the expression vector comprises: a) a transcription initiation region; b) a transcription termination region; c) an open reading frame; and d) a nucleic acid sequence encoding at least one strand of a siNA molecule, wherein the sequence is operably linked to the 3'-end of the open reading frame and wherein the sequence is operably linked to the initiation region, the open reading frame and the termination region in a manner that allows expression and/or delivery of the siNA molecule. In yet another embodiment, the expression vector comprises: a) a transcription initiation region; b) a transcription termination region; c) an intron; and d) a nucleic acid sequence encoding at least one siNA molecule, wherein the sequence is operably linked to the initiation region, the intron and the termination region in a manner which allows expression and/or delivery of the nucleic acid molecule.

In another embodiment, the expression vector comprises: a) a transcription initiation region; b) a transcription termination region; c) an intron; d) an open reading frame; and e) a nucleic acid sequence encoding at least one strand of a siNA molecule, wherein the sequence is operably linked to the 3'-end of the open reading frame and wherein the sequence is operably linked to the initiation region, the intron, the open

reading frame and the termination region in a manner which allows expression and/or delivery of the siNA molecule.

PDGF/PDGFr biology and biochemistry

The following discussion is adapted from R&D Systems Mini-Reviews and Tech Notes, Cytokine Mini-Reviews, Platelet Derived Growth Factor, Copyright ©2002 R&D Systems. Historically, it has been a goal of tissue culture researchers to identify substances that provide universal growth or maintenance factor characteristics for various cell lines and isolates. Early tissue culture work demonstrated the superiority of serum over plasma in stimulating the proliferation of fibroblasts in vitro. These observations suggested that a factor released from platelets during degranulation was probably responsible for the stimulatory activity. Subsequent investigations clearly demonstrated that a certain factor released from platelets upon clotting was capable of promoting the growth of various types of cells. This factor was subsequently purified from platelets and given the name platelet-derived growth factor (PDGF). PDGF is now known to be produced by a number of cell types besides platelets and it has been found to be a mitogen for almost all mesenchymally-derived cells, such as blood, muscle, bone/cartilage, and connective tissue cells.

Three forms of PDGF have been identified to date. Each form consists of a 30 kDa homo- or heterodimeric combination of two genetically distinct, but structurally related, polypeptide chains which are designated A and B chains, respectively. Although considerable work has been done on the primary structure of each of the chains of human PDGF, the process has been complicated by the fact that each is synthesized as a propeptide, that splice variants exist for the A chain, and that C-terminal proteolytic processing apparently occurs for the B chain and possibly the A chain as well.

The PDGF A chain is the product of a seven exon chromosomal 7 gene that gives rise to one of two distinct splice variants. The "long" variant, a prepropeptide of 211 amino acid residues, is synthesized with a signal peptide of 20 amino acid residues, a propeptide sequence of 66 amino acid residues, and a mature chain of 125 amino acid residues. In contrast, the "short" 196 amino acid residue variant shows a 20 amino acid residue signal sequence, a 66 amino acid residue propeptide, and a 16-18 kDa, 110 amino acid residue mature form. The difference between the long and short results from

alternative exon usage, with the extended form utilizing exon 6 (18 amino acid residues), but not exon 7, and the short form utilizing exon 7 (3 amino acid residues), but not exon 6. The difference between exon 6 utilization and exon 7 utilization is not, however, limited to length. Within the 18 amino acid residues of exon 6 lies an approximately 10 amino acid residue sequence that signals cell retention. Failure to remove this carboxyterminal peptide results in a failure to release freely circulating PDGF. Retention under these circumstances implies binding to either cell-surface glycosaminoglycans or intercellular matrix. The short version contains no retention sequence and is secreted into the circulatory system. It is presently unclear whether any C-terminal processing of A chains occurs, but the short variant's 110 amino acid residue mature peptide terminates with an arginine residue. This suggests the possibility, as is the case for the B chain, of a carboxypeptidase-mediated C-terminal truncation to 109 amino acid residues with equilization of A and B chain lengths for dimerization. No definitive mechanism for C-terminus processing of the long form of the A chain has been elucidated and it is not presently clear if this form is secreted. One potential N-linked glycosylation site exists in the mature A chain, but not the B chain, and it is suggested to be utilized. Normal cells such as endothelial cell, macrophages, and fibroblasts are known to concurrently express both types of A chain, with the short version being the most abundant.

The PDGF B chain is the product of a six exon gene on chromosome 22. The B chain gene is known to be identical to the human c-sis gene, the normal human cell counterpart to the monkey v-sis (simian sarcoma) virus gene. The protein coded for by c-sis is a 27 kDa, 241 amino acid residue prepropeptide with a 20 amino acid residue signal sequence, 61 amino acid residue propeptide, and a 16 kDa, 160 amino acid residue "mature" polypeptide. C-terminal cleavage of the mature B chain is believed to occur, resulting in a final mature product of 12 kDa and 109 amino acid residues. This is proposed to occur in two stages with a trypsin-like cleavage of residues 111 to 160, followed by a carboxypeptidase cleavage of the remaining arginine at residue 110. As with the long form of chain A, a particular retention sequence approximately 10 amino acid residues in length has also been identified in the B chain C-terminus. Failure to remove this peptide also results in B chain glycosaminoglycan retention. Dimerization of the A and B chains involves two interchain disulfide bonds, and each chain overlaps the

other with a 6 or 7 amino acid residue extension at either end. Within the 103 overlapping amino acid residues, the two chains exhibit about 50% sequence identity.

Cells known to express PDGF are diverse. Cells that are reported to express the A chain protein (both long and short variants) include fibroblasts, endothelial cells, 5 osteoblasts, platelets, vascular smooth muscle cells, macrophages and Langerhans cells, and fetal fibroblasts. Cells producing B chain protein include fetal fibroblasts, endothelial cells, platelets, macrophages, neurons and breast ductal epithelium. A number of cell types have also been shown to express mRNA for the PDGF chains. In particular, A chain mRNA has been found in type I astrocytes, embryonic endodermal respiratory 10 epithelium, renal mesangial cells, and osteoclasts and chondrocytes, while B chain mRNA has been localized to embryonic endodermal respiratory epithelium, renal mesangial cells and osteoblasts.

As with many growth factors, PDGF is now considered to be a member of a larger family of factors. In addition to PDGF, this family includes the homodimeric factors 15 VEGF (vascular endothelial growth factor) and PlGF (placental growth factor), VEGF/PlGF heterodimers, and CTGF (connective tissue growth factor), a PDGF-like factor secreted by human vascular endothelial cells and fibroblasts. Relative to the PDGF isoforms, VEGF shows distant analogy to PDGF-BB while PlGF corresponds to PDGF-AA. CTGF shows little amino acid identity with PDGF A or B, but reacts with antisera 20 produced against PDGF. Recently, the status of PDGF has been re-evaluated based on analysis of its 3-dimensional structure. Along with NGF, TGF-beta and glycoprotein hormones (human chorionic gonadotrophic), PDGF is now classified as a member of the cysteine-knot growth factor superfamily. Each member of this group occurs as a dimer and is characterized by six cysteines which link together to form a "molecular knot". The 25 existence of this knot is only revealed by 3-D analysis, making the criteria for admission to this family unique among superfamilies.

An association is known to exist between alpha-2 macroglobulin (alpha-2M) and the B chain-containing PDGF forms, AB and BB. alpha-2M is a circulating 720 kDa homotetrameric glycoprotein produced by hepatocytes, macrophages and astrocytes 30 whose most widely reported function is that of a scavenger of proteases. Although PDGF does not interact with the region associated with protease entrapment, it does bind to

other alpha-2M sites not influenced by activation. PDGF-BB has been noted to bind to both fast and slow alpha-2M and does so principally in a noncovalent manner. Significantly, the binding is reversible, and PDGF dissociation is suggested to occur at either low pH or when equilibrium kinetics favor dissociation, such as might be the case when PDGF is removed from circulation by binding to its own receptors. Functionally, it is not clear what the role is for B chain binding to alpha-2M. PDGF binding to the slow form seems to result in its storage, as the alpha-2M receptor binding motif(s) are not exposed, and the PDGF-alpha-2M complex simply circulates. On the other hand, binding to fast or activated alpha-2M results in its rapid clearance via alpha-2M receptors, bringing the PDGF molecule close to its own receptors and perhaps facilitating a secondary PDGF-PDGFR interaction.

Two distinct human PDGF receptor transmembrane binding proteins have been identified, a 170 kDa, 1066 amino acid residue alpha-receptor (PDGFR alpha) and a 190 kDa, 1074 amino acid residue beta-receptor (PDGFR beta). The two receptor proteins are structurally related and consist of an extracellular portion containing five immunoglobulin-like domains, a single transmembrane region, and an intracellular portion with a protein-tyrosine kinase domain. A functional PDGF receptor is formed when the two chains of a dimeric PDGF molecule each bind one of the above receptor molecules, resulting in their approximation, dimerization and activation. Between the two proteins, there is 44% overall sequence identity. Within the extracellular domain, 30% of the amino acid residues are identical. In addition, a 90 kDa soluble form of PDGFR alpha, consisting of the extracellular segment of the alpha-receptor, has been found in cell culture medium and in human plasma. The above two transmembrane receptors share characteristics with other growth factor receptors, such as the M-CSF receptor, c-kit, and the FGF receptor family. High-affinity binding of PDGF involves dimerization of the receptors, forming either homodimers or heterodimers with the alpha and beta receptors/chains. Although it appears that each subunit of dimeric PDGF binds to one receptor monomer, it is unclear if these PDGF subunits need to be covalently linked. Recent evidence suggests noncovalently linked B chains are able to activate the PDGFR.

PDGFR alpha binds each of the three forms of PDGF dimers with high affinity. Although PDGFR beta binds both PDGF-BB and PDGF-AB with high affinity, it has no reported binding to PDGF-AA. The apparent high-affinity binding of the AB dimer to

the beta-receptor must be interpreted with caution, however. Although PDGF-AB can bind to mutant 3T3 cells displaying only beta-receptors, it requires 100-fold more PDGF-AB to dimerize the beta-receptors and activate the cells than is required for cells also displaying alpha-receptors. Cells known to express only alpha-receptors include oligodendroglial progenitors, liver endothelial cells and mesothelium, and platelets. Cells expressing only beta-receptors include CNS capillary endothelium, neurons and Ito (fat storing) cells of the liver, plus monocytes/macrophages. Cells showing coincident expression of alpha and beta receptors include smooth muscle cells, fibroblasts, and Schwann cells.

Receptor binding by PDGF is known to activate intracellular tyrosine kinase, leading to autophosphorylation of the cytoplasmic domain of the receptor as well as phosphorylation of other intracellular substrates. This reaction is described as one in trans, i.e., the two receptor molecules of the receptor dimer phosphorylate each other. Specific substrates identified with the beta-receptor include Src, GTPase Activating Protein (GAP), phospholipase C γ (PLC γ) and phosphatidylinositol 3-phosphate. Both PLC γ and GAP seem to bind with different affinities to the α - and beta-receptors, suggesting that the particular response of a cell depends on the type of receptor it expresses and the type of PDGF dimer to which it is exposed. In addition to the above, a non-tyrosine phosphorylation-associated signal transduction pathway can also be activated that involves the zinc finger protein erg-1 (early growth response gene 1).

Because there are differences between cells relative to the amounts of alpha- and beta-receptors that they express, and because of the variability in PDGF isomer binding to receptors, there is a large range of possibilities for biological responses by PDGF. This is reflected in at least four experimental systems where different isoforms of PDGF elicit different results. Vascular smooth muscle cells (SMC) and fibroblasts are both known to express both the alpha- and beta-receptors. In SMC, PDGF-AA initiates cellular hypertrophy (increased protein synthesis), while BB induces hyperplasia (mitosis). In fibroblasts, the BB isoform initiates chemotaxis, while AA inhibits chemotaxis. In dopaminergic neurons, PDGF-AA promotes embryonic neuron fiber development, while BB serves only as a survival or maintenance factor. Finally, within the developing lung, the BB isoform regulates the growth and number of respiratory tubule epithelial cells,

while the AA isoform directs the actual formation of branches arising from the respiratory tubules.

In general, PDGF isoforms are potent mitogens for connective tissue cells, including dermal fibroblasts, arterial smooth muscle cells, chondrocytes and some epithelial and endothelial cells. In addition to its activity as a mitogen, PDGF is chemotactic for fibroblasts and smooth muscle cells, cells which also respond mitogenically to PDGF, and for neutrophils and mononuclear cells, cells for which PDGF is not a mitogen. There is a considerable body of evidence to indicate that PDGF derived from macrophages, acting as a chemotactic and mitogenic agent for smooth muscle cells, contributes to the myointimal thickening of arterial walls characteristic of atherosclerosis. Other reported activities for PDGF include the stimulation of granule release by neutrophils and monocytes, the facilitation of steroid synthesis by Leydig cells, stimulation of neutrophil phagocytosis, modulation of thrombospondin expression and secretion, upregulation of ICAM-1 in vascular smooth muscle cells, and the transient induction of T cell IL-2 secretion, accompanied by a down-regulation of IL-4 and IFN-gamma production, which allow clonal expansion of antigen-activated B and T helper lymphocytes prior to differentiation. PDGF also appears to be ubiquitous in neurons throughout the CNS, where it is suggested to play an important role in neuron survival and regeneration, and in mediation of glial cell proliferation, differentiation and migration.

The use of small interfering nucleic acid molecules targeting PDGF and its receptors therefore provides a class of novel therapeutic agents that can be used in the treatment of cancers, proliferative diseases (e.g., restenosis), inflammatory disease, or any other disease or condition that responds to modulation of PDGF and PDGFr genes.

25 Examples:

The following are non-limiting examples showing the selection, isolation, synthesis and activity of nucleic acids of the instant invention.

Example 1: Tandem synthesis of siNA constructs

Exemplary siNA molecules of the invention are synthesized in tandem using a cleavable linker, for example a succinyl-based linker. Tandem synthesis as described herein is followed by a one-step purification process that provides RNAi molecules in high yield. This approach is highly amenable to siNA synthesis in support of high throughput RNAi screening, and can be readily adapted to multi-column or multi-well synthesis platforms.

After completing a tandem synthesis of a siNA oligo and its complement in which the 5'-terminal dimethoxytrityl (5'-O-DMT) group remains intact (trityl on synthesis), the oligonucleotides are deprotected as described above. Following deprotection, the siNA sequence strands are allowed to spontaneously hybridize. This hybridization yields a duplex in which one strand has retained the 5'-O-DMT group while the complementary strand comprises a terminal 5'-hydroxyl. The newly formed duplex behaves as a single molecule during routine solid-phase extraction purification (Trityl-On purification) even though only one molecule has a dimethoxytrityl group. Because the strands form a stable duplex, this dimethoxytrityl group (or an equivalent group, such as other trityl groups or other hydrophobic moieties) is all that is required to purify the pair of oligos, for example by using a C18 cartridge.

Standard phosphoramidite synthesis chemistry is used up to the point of introducing a tandem linker, such as an inverted deoxy abasic succinate or glyceryl succinate linker (see **Figure 1**) or an equivalent cleavable linker. A non-limiting example of linker coupling conditions that can be used includes a hindered base such as diisopropylethylamine (DIPA) and/or DMAP in the presence of an activator reagent such as Bromotripyrrolidinophosphoniumhexafluorophosphate (PyBrOP). After the linker is coupled, standard synthesis chemistry is utilized to complete synthesis of the second sequence leaving the terminal the 5'-O-DMT intact. Following synthesis, the resulting oligonucleotide is deprotected according to the procedures described herein and quenched with a suitable buffer, for example with 50mM NaOAc or 1.5M $\text{NH}_4\text{H}_2\text{CO}_3$.

Purification of the siNA duplex can be readily accomplished using solid phase extraction, for example using a Waters C18 SepPak 1g cartridge conditioned with 1

column volume (CV) of acetonitrile, 2 CV H₂O, and 2 CV 50mM NaOAc. The sample is loaded and then washed with 1 CV H₂O or 50mM NaOAc. Failure sequences are eluted with 1 CV 14% ACN (Aqueous with 50mM NaOAc and 50mM NaCl). The column is then washed, for example with 1 CV H₂O followed by on-column detritylation, for example by passing 1 CV of 1% aqueous trifluoroacetic acid (TFA) over the column, then adding a second CV of 1% aqueous TFA to the column and allowing to stand for approximately 10 minutes. The remaining TFA solution is removed and the column washed with H₂O followed by 1 CV 1M NaCl and additional H₂O. The siNA duplex product is then eluted, for example using 1 CV 20% aqueous CAN.

Figure 2 provides an example of MALDI-TOV mass spectrometry analysis of a purified siNA construct in which each peak corresponds to the calculated mass of an individual siNA strand of the siNA duplex. The same purified siNA provides three peaks when analyzed by capillary gel electrophoresis (CGE), one peak presumably corresponding to the duplex siNA, and two peaks presumably corresponding to the separate siNA sequence strands. Ion exchange HPLC analysis of the same siNA construct only shows a single peak. Testing of the purified siNA construct using a luciferase reporter assay described below demonstrated the same RNAi activity compared to siNA constructs generated from separately synthesized oligonucleotide sequence strands.

Example 2: Identification of potential siNA target sites in any RNA sequence

The sequence of an RNA target of interest, such as a viral or human mRNA transcript, is screened for target sites, for example by using a computer folding algorithm. In a non-limiting example, the sequence of a gene or RNA gene transcript derived from a database, such as Genbank, is used to generate siNA targets having complementarity to the target. Such sequences can be obtained from a database, or can be determined experimentally as known in the art. Target sites that are known, for example, those target sites determined to be effective target sites based on studies with other nucleic acid molecules, for example ribozymes or antisense, or those targets known to be associated with a disease or condition such as those sites containing mutations or deletions, can be used to design siNA molecules targeting those sites. Various parameters can be used to determine which sites are the most suitable target sites within the target RNA sequence. These parameters include but are not limited to secondary or tertiary RNA structure, the

nucleotide base composition of the target sequence, the degree of homology between various regions of the target sequence, or the relative position of the target sequence within the RNA transcript. Based on these determinations, any number of target sites within the RNA transcript can be chosen to screen siNA molecules for efficacy, for example by using *in vitro* RNA cleavage assays, cell culture, or animal models. In a non-limiting example, anywhere from 1 to 1000 target sites are chosen within the transcript based on the size of the siNA construct to be used. High throughput screening assays can be developed for screening siNA molecules using methods known in the art, such as with multi-well or multi-plate assays to determine efficient reduction in target gene expression.

10 Example 3: Selection of siNA molecule target sites in a RNA

The following non-limiting steps can be used to carry out the selection of siNAs targeting a given gene sequence or transcript.

1. The target sequence is parsed *in silico* into a list of all fragments or subsequences of a particular length, for example 23 nucleotide fragments, contained within the target sequence. This step is typically carried out using a custom Perl script, but commercial sequence analysis programs such as Oligo, MacVector, or the GCG Wisconsin Package can be employed as well.
2. In some instances the siNAs correspond to more than one target sequence; such would be the case for example in targeting different transcripts of the same gene, targeting different transcripts of more than one gene, or for targeting both the human gene and an animal homolog. In this case, a subsequence list of a particular length is generated for each of the targets, and then the lists are compared to find matching sequences in each list. The subsequences are then ranked according to the number of target sequences that contain the given subsequence; the goal is to find subsequences that are present in most or all of the target sequences. Alternately, the ranking can identify subsequences that are unique to a target sequence, such as a mutant target sequence. Such an approach would enable the use of siNA to target specifically the mutant sequence and not effect the expression of the normal sequence.
3. In some instances the siNA subsequences are absent in one or more sequences while present in the desired target sequence; such would be the case if the siNA targets a

gene with a paralogous family member that is to remain untargeted. As in case 2 above, a subsequence list of a particular length is generated for each of the targets, and then the lists are compared to find sequences that are present in the target gene but are absent in the untargeted paralog.

- 5 4. The ranked siNA subsequences can be further analyzed and ranked according to GC content. A preference can be given to sites containing 30-70% GC, with a further preference to sites containing 40-60% GC.
- 10 5. The ranked siNA subsequences can be further analyzed and ranked according to self-folding and internal hairpins. Weaker internal folds are preferred; strong hairpin structures are to be avoided.
- 15 6. The ranked siNA subsequences can be further analyzed and ranked according to whether they have runs of GGG or CCC in the sequence. GGG (or even more Gs) in either strand can make oligonucleotide synthesis problematic and can potentially interfere with RNAi activity, so it is avoided whenever better sequences are available. CCC is searched in the target strand because that will place GGG in the antisense strand.
- 20 7. The ranked siNA subsequences can be further analyzed and ranked according to whether they have the dinucleotide UU (uridine dinucleotide) on the 3'-end of the sequence, and/or AA on the 5'-end of the sequence (to yield 3' UU on the antisense sequence). These sequences allow one to design siNA molecules with terminal TT thymidine dinucleotides.
- 25 8. Four or five target sites are chosen from the ranked list of subsequences as described above. For example, in subsequences having 23 nucleotides, the right 21 nucleotides of each chosen 23-mer subsequence are then designed and synthesized for the upper (sense) strand of the siNA duplex, while the reverse complement of the left 21 nucleotides of each chosen 23-mer subsequence are then designed and synthesized for the lower (antisense) strand of the siNA duplex (see **Tables II and III**). If terminal TT residues are desired for the sequence (as described in paragraph 7), then the two 3' terminal nucleotides of both the sense and antisense strands are replaced by TT prior to synthesizing the oligos.
- 30

9. The siNA molecules are screened in an *in vitro*, cell culture or animal model system to identify the most active siNA molecule or the most preferred target site within the target RNA sequence.

In an alternate approach, a pool of siNA constructs specific to a PDGF and/or PDGFr target sequence is used to screen for target sites in cells expressing PDGF and/or PDGFr RNA, such as human aortic smooth muscle cells (e.g., HASMC), HeLa cells, or A549 cells. The general strategy used in this approach is shown in **Figure 9**. A non-limiting example of such as pool is a pool comprising sequences having sense sequences comprising SEQ ID NOs. 1-311, 623-630, 635-638, and 643-646 and antisense sequences comprising SEQ ID NOs. 312-622, 631-634, 639-642, and 647-650 respectively. Cells expressing PDGF and/or PDGFr (e.g., HASMC, HeLa, or A549 cells), are transfected with the pool of siNA constructs and cells that demonstrate a phenotype associated with PDGF and/or PDGFr inhibition are sorted. The pool of siNA constructs can be expressed from transcription cassettes inserted into appropriate vectors (see for example **Figure 7** and **Figure 8**). The siNA from cells demonstrating a positive phenotypic change (e.g., decreased proliferation, decreased PDGF and/or PDGFr mRNA levels or decreased PDGF and/or PDGFr protein expression), are sequenced to determine the most suitable target site(s) within the target PDGF and/or PDGFr RNA sequence.

Example 4: PDGF and/or PDGFr targeted siNA design

siNA target sites were chosen by analyzing sequences of the PDGF and/or PDGFr RNA target and optionally prioritizing the target sites on the basis of folding (structure of any given sequence analyzed to determine siNA accessibility to the target), by using a library of siNA molecules as described in Example 3, or alternately by using an *in vitro* siNA system as described in Example 6 herein. siNA molecules were designed that could bind each target and are optionally individually analyzed by computer folding to assess whether the siNA molecule can interact with the target sequence. Varying the length of the siNA molecules can be chosen to optimize activity. Generally, a sufficient number of complementary nucleotide bases are chosen to bind to, or otherwise interact with, the target RNA, but the degree of complementarity can be modulated to accommodate siNA duplexes or varying length or base composition. By using such methodologies, siNA

molecules can be designed to target sites within any known RNA sequence, for example those RNA sequences corresponding to the any gene transcript.

Chemically modified siNA constructs are designed to provide nuclease stability for systemic administration in vivo and/or improved pharmacokinetic, localization, and delivery properties while preserving the ability to mediate RNAi activity. Chemical modifications as described herein are introduced synthetically using synthetic methods described herein and those generally known in the art. The synthetic siNA constructs are then assayed for nuclease stability in serum and/or cellular/tissue extracts (e.g. liver extracts). The synthetic siNA constructs are also tested in parallel for RNAi activity using an appropriate assay, such as a luciferase reporter assay as described herein or another suitable assay that can quantify RNAi activity. Synthetic siNA constructs that possess both nuclease stability and RNAi activity can be further modified and re-evaluated in stability and activity assays. The chemical modifications of the stabilized active siNA constructs can then be applied to any siNA sequence targeting any chosen RNA and used, for example, in target screening assays to pick lead siNA compounds for therapeutic development (see for example **Figure 11**).

Example 5: Chemical Synthesis and Purification of siNA

siNA molecules can be designed to interact with various sites in the RNA message, for example target sequences within the RNA sequences described herein. The sequence of one strand of the siNA molecule(s) is complementary to the target site sequences described above. The siNA molecules can be chemically synthesized using methods described herein. Inactive siNA molecules that are used as control sequences can be synthesized by scrambling the sequence of the siNA molecules such that it is not complementary to the target sequence. Generally, siNA constructs can be synthesized using solid phase oligonucleotide synthesis methods as described herein (see for example Usman *et al.*, US Patent Nos. 5,804,683; 5,831,071; 5,998,203; 6,117,657; 6,353,098; 6,362,323; 6,437,117; 6,469,158; Scaringe *et al.*, US Patent Nos. 6,111,086; 6,008,400; 6,111,086 all incorporated by reference herein in their entirety).

In a non-limiting example, RNA oligonucleotides are synthesized in a stepwise fashion using the phosphoramidite chemistry as is known in the art. Standard phosphoramidite chemistry involves the use of nucleosides comprising any of 5'-O-

dimethoxytrityl, 2'-O-tert-butyldimethylsilyl, 3'-O-2-Cyanoethyl N,N-diisopropylphosphoramidite groups, and exocyclic amine protecting groups (e.g. N6-benzoyl adenosine, N4 acetyl cytidine, and N2-isobutyryl guanosine). Alternately, 2'-O-Silyl Ethers can be used in conjunction with acid-labile 2'-O-orthoester protecting groups in the synthesis of
5 RNA as described by Scaringe *supra*. Differing 2' chemistries can require different protecting groups, for example 2'-deoxy-2'-amino nucleosides can utilize N-phthaloyl protection as described by Usman *et al.*, US Patent 5,631,360, incorporated by reference herein in its entirety).

During solid phase synthesis, each nucleotide is added sequentially (3'- to 5'-
10 direction) to the solid support-bound oligonucleotide. The first nucleoside at the 3'-end of the chain is covalently attached to a solid support (e.g., controlled pore glass or polystyrene) using various linkers. The nucleotide precursor, a ribonucleoside phosphoramidite, and activator are combined resulting in the coupling of the second nucleoside phosphoramidite onto the 5'-end of the first nucleoside. The support is then
15 washed and any unreacted 5'-hydroxyl groups are capped with a capping reagent such as acetic anhydride to yield inactive 5'-acetyl moieties. The trivalent phosphorus linkage is then oxidized to a more stable phosphate linkage. At the end of the nucleotide addition cycle, the 5'-O-protecting group is cleaved under suitable conditions (e.g., acidic conditions for trityl-based groups and Fluoride for silyl-based groups). The cycle is
20 repeated for each subsequent nucleotide.

Modification of synthesis conditions can be used to optimize coupling efficiency, for example by using differing coupling times, differing reagent/phosphoramidite concentrations, differing contact times, differing solid supports and solid support linker chemistries depending on the particular chemical composition of the siNA to be
25 synthesized. Deprotection and purification of the siNA can be performed as is generally described in Vargeese *et al.*, USSN 10/194,875 incorporated by reference herein in its entirety or Scaringe *supra*. Additionally, deprotection conditions can be modified to provide the best possible yield and purity of siNA constructs. For example, applicant has observed that oligonucleotides comprising 2'-deoxy-2'-fluoro nucleotides can degrade
30 under inappropriate deprotection conditions. Such oligonucleotides are deprotected using aqueous methylamine at about 35°C for 30 minutes. If the 2'-deoxy-2'-fluoro containing oligonucleotide also comprises ribonucleotides, after deprotection with aqueous

methylamine at about 35°C for 30 minutes, TEA-HF is added and the reaction maintained at about 65°C for an additional 15 minutes.

Example 6: RNAi *in vitro* assay to assess siNA activity

An *in vitro* assay that recapitulates RNAi in a cell-free system is used to evaluate siNA constructs targeting PDGF and/or PDGFr RNA targets. The assay comprises the system described by Tuschl *et al.*, 1999, *Genes and Development*, 13, 3191-3197 and Zamore *et al.*, 2000, *Cell*, 101, 25-33 adapted for use with PDGF and/or PDGFr target RNA. A *Drosophila* extract derived from syncytial blastoderm is used to reconstitute RNAi activity *in vitro*. Target RNA is generated via *in vitro* transcription from an appropriate PDGF and/or PDGFr expressing plasmid using T7 RNA polymerase or via chemical synthesis as described herein. Sense and antisense siNA strands (for example 20 uM each) are annealed by incubation in buffer (such as 100 mM potassium acetate, 30 mM HEPES-KOH, pH 7.4, 2 mM magnesium acetate) for 1 min. at 90°C followed by 1 hour at 37°C, then diluted in lysis buffer (for example 100 mM potassium acetate, 30 mM HEPES-KOH at pH 7.4, 2mM magnesium acetate). Annealing can be monitored by gel electrophoresis on an agarose gel in TBE buffer and stained with ethidium bromide. The *Drosophila* lysate is prepared using zero to two-hour-old embryos from Oregon R flies collected on yeasted molasses agar that are dechorionated and lysed. The lysate is centrifuged and the supernatant isolated. The assay comprises a reaction mixture containing 50% lysate [vol/vol], RNA (10-50 pM final concentration), and 10% [vol/vol] lysis buffer containing siNA (10 nM final concentration). The reaction mixture also contains 10 mM creatine phosphate, 10 ug/ml creatine phosphokinase, 100 uM GTP, 100 uM UTP, 100 uM CTP, 500 uM ATP, 5 mM DTT, 0.1 U/uL RNasin (Promega), and 100 uM of each amino acid. The final concentration of potassium acetate is adjusted to 100 mM. The reactions are pre-assembled on ice and preincubated at 25° C for 10 minutes before adding RNA, then incubated at 25° C for an additional 60 minutes. Reactions are quenched with 4 volumes of 1.25 x Passive Lysis Buffer (Promega). Target RNA cleavage is assayed by RT-PCR analysis or other methods known in the art and are compared to control reactions in which siNA is omitted from the reaction.

Alternately, internally-labeled target RNA for the assay is prepared by *in vitro* transcription in the presence of [α -³²P] CTP, passed over a G 50 Sephadex column by

spin chromatography and used as target RNA without further purification. Optionally, target RNA is 5'-³²P-end labeled using T4 polynucleotide kinase enzyme. Assays are performed as described above and target RNA and the specific RNA cleavage products generated by RNAi are visualized on an autoradiograph of a gel. The percentage of cleavage is determined by Phosphor Imager[®] quantitation of bands representing intact control RNA or RNA from control reactions without siNA and the cleavage products generated by the assay.

In one embodiment, this assay is used to determine target sites the PDGF and/or PDGFr RNA target for siNA mediated RNAi cleavage, wherein a plurality of siNA constructs are screened for RNAi mediated cleavage of the PDGF and/or PDGFr RNA target, for example by analyzing the assay reaction by electrophoresis of labeled target RNA, or by northern blotting, as well as by other methodology well known in the art.

Example 7: Nucleic acid inhibition of PDGF and/or PDGFr target RNA *in vivo*

siNA molecules targeted to the human PDGF and/or PDGFr RNA are designed and synthesized as described above. These nucleic acid molecules can be tested for cleavage activity *in vivo*, for example, using the following procedure. The target sequences and the nucleotide location within the PDGF and/or PDGFr RNA are given in **Table II and III**.

Two formats are used to test the efficacy of siNAs targeting PDGF and/or PDGFr. First, the reagents are tested in cell culture using, for example, HASMC, HeLa, or A549 cells to determine the extent of RNA and protein inhibition. siNA reagents (*e.g.*; see **Tables II and III**) are selected against the PDGF and/or PDGFr target as described herein. RNA inhibition is measured after delivery of these reagents by a suitable transfection agent to, for example, HASMC, HeLa, or A549 cells. Relative amounts of target RNA are measured versus actin using real-time PCR monitoring of amplification (*eg.*, ABI 7700 Taqman[®]). A comparison is made to a mixture of oligonucleotide sequences made to unrelated targets or to a randomized siNA control with the same overall length and chemistry, but randomly substituted at each position. Primary and secondary lead reagents are chosen for the target and optimization performed. After an optimal transfection agent concentration is chosen, a RNA time-course of inhibition is

performed with the lead siNA molecule. In addition, a cell-plating format can be used to determine RNA inhibition.

Delivery of siNA to Cells

Cells (e.g., HASMC, HeLa, or A549 cells) are seeded, for example, at 1×10^5 cells per well of a six-well dish in EGM-2 (BioWhittaker) the day before transfection. siNA (final concentration, for example 20nM) and cationic lipid (e.g., final concentration 2 μ g/ml) are complexed in EGM basal media (Biowhittaker) at 37°C for 30 mins in polystyrene tubes. Following vortexing, the complexed siNA is added to each well and incubated for the times indicated. For initial optimization experiments, cells are seeded, for example, at 1×10^3 in 96 well plates and siNA complex added as described. Efficiency of delivery of siNA to cells is determined using a fluorescent siNA complexed with lipid. Cells in 6-well dishes are incubated with siNA for 24 hours, rinsed with PBS and fixed in 2% paraformaldehyde for 15 minutes at room temperature. Uptake of siNA is visualized using a fluorescent microscope.

Taqman and Lightcycler quantification of mRNA

Total RNA is prepared from cells following siNA delivery, for example using Qiagen RNA purification kits for 6-well or Rneasy extraction kits for 96-well assays. For Taqman analysis, dual-labeled probes are synthesized with the reporter dye, FAM or JOE, covalently linked at the 5'-end and the quencher dye TAMRA conjugated to the 3'-end. One-step RT-PCR amplifications are performed on, for example, an ABI PRISM 7700 Sequence Detector using 50 μ l reactions consisting of 10 μ l total RNA, 100 nM forward primer, 900 nM reverse primer, 100 nM probe, 1X TaqMan PCR reaction buffer (PE-Applied Biosystems), 5.5 mM MgCl₂, 300 μ M each dATP, dCTP, dGTP, and dTTP, 10U RNase Inhibitor (Promega), 1.25U AmpliTaq Gold (PE-Applied Biosystems) and 10U M-MLV Reverse Transcriptase (Promega). The thermal cycling conditions can consist of 30 min at 48°C, 10 min at 95°C, followed by 40 cycles of 15 sec at 95°C and 1 min at 60°C. Quantitation of mRNA levels is determined relative to standards generated from serially diluted total cellular RNA (300, 100, 33, 11 ng/rxn) and normalizing to β -actin or GAPDH mRNA in parallel TaqMan reactions. For each gene of interest an upper and lower primer and a fluorescently labeled probe are designed. Real time incorporation of

SYBR Green I dye into a specific PCR product can be measured in glass capillary tubes using a lightcycler. A standard curve is generated for each primer pair using control cRNA. All values are represented as relative expression to GAPDH in each sample.

Western blotting

5 Nuclear extracts can be prepared using a standard micro preparation technique (see for example Andrews and Faller, 1991, *Nucleic Acids Research*, 19, 2499). Protein extracts from supernatants are prepared, for example using TCA precipitation. An equal volume of 20% TCA is added to the cell supernatant, incubated on ice for 1 hour and pelleted by centrifugation for 5 minutes. Pellets are washed in acetone, dried and
10 resuspended in water. Cellular protein extracts are run on a 10% Bis-Tris NuPage (nuclear extracts) or 4-12% Tris-Glycine (supernatant extracts) polyacrylamide gel and transferred onto nitro-cellulose membranes. Non-specific binding can be blocked by incubation, for example, with 5% non-fat milk for 1 hour followed by primary antibody for 16 hour at 4°C. Following washes, the secondary antibody is applied, for example
15 (1:10,000 dilution) for 1 hour at room temperature and the signal detected with SuperSignal reagent (Pierce).

Example 8: Models useful to evaluate the down-regulation of PDGF and/or PDGFr gene expression

Cell Culture

20 There are numerous cell culture systems that can be used to analyze reduction of PDGF and/or PDGFr levels either directly or indirectly by measuring downstream effects. For example, HASMC, HeLa, or A549 cells can be used in cell culture experiments to assess the efficacy of nucleic acid molecules of the invention. As such, HASMC, HeLa, or A549 cells treated with nucleic acid molecules of the invention (e.g., siNA) targeting
25 PDGF and/or PDGFr RNA would be expected to have decreased PDGF and/or PDGFr expression capacity following stimulation with pro-inflammatory cytokines compared to matched control nucleic acid molecules having a scrambled or inactive sequence. In a non-limiting example, HASMC, HeLa, or A549 cells are cultured and PDGF and/or PDGFr expression is quantified, for example by time-resolved immunofluorometric
30 assay. PDGF and/or PDGFr messenger-RNA expression is quantitated with RT-PCR in

cultured cells. Untreated cells are compared to cells treated with siNA molecules transfected with a suitable reagent, for example, a cationic lipid such as lipofectamine, and PDGF and/or PDGFr protein and RNA levels are quantitated. Dose response assays are then performed to establish dose dependent inhibition of PDGF and/or PDGFr expression.

In several cell culture systems, cationic lipids have been shown to enhance the bioavailability of oligonucleotides to cells in culture (Bennet, *et al.*, 1992, *Mol. Pharmacology*, 41, 1023-1033). In one embodiment, siNA molecules of the invention are complexed with cationic lipids for cell culture experiments. siNA and cationic lipid mixtures are prepared in serum-free DMEM immediately prior to addition to the cells. DMEM plus additives are warmed to room temperature (about 20-25°C) and cationic lipid is added to the final desired concentration and the solution is vortexed briefly. siNA molecules are added to the final desired concentration and the solution is again vortexed briefly and incubated for 10 minutes at room temperature. In dose response experiments, the RNA/lipid complex is serially diluted into DMEM following the 10 minute incubation.

Animal Models

Evaluating the efficacy of anti-PDGF and/or PDGFr agents in animal models is an important prerequisite to human clinical trials. Barisoni *et al.*, 1995, *Am J Pathol.*, 147, 1728-35 describe a transgenic mouse model of polycystic kidney disease. Adult polycystic kidney disease is believed to be the most frequent (1/500) inherited genetic disorder in humans. Barisoni *et al.*, *supra* generated a genetic model of the disease in transgenic mice by introducing a deregulated proto-oncogene *c-myc* specifically expressed in the kidney. All transgenic lines produced develop adult polycystic kidney disease in a reproducible manner. The clinical phenotype observed in mice is present at birth and leads to renal insufficiency in adulthood. Barisoni *et al.*, *supra* determined that abnormal proliferation and programmed cell death are responsible for cystogenesis in polycystic kidney disease. Furthermore, this phenomena is controlled by a specific *c-myc* mechanism independent of the p53 pathway. A similar mechanism also prevails in human autosomal dominant polycystic kidney disease. Therefore, this murine model

provides a useful model to understand the polycystic kidney disease pathogenesis and can be used to evaluate potential therapeutic agents such as siNA molecules of the invention.

Other animal models known in the art can be used to evaluate siNA molecules of the invention targeting PDGF and PDGFr for other disease conditions, see for example
5 *Karas et al.*, 1992, Coronary intimal proliferation after balloon injury and stenting in swine: An animal model of restenosis. *J Am Coll Cardiol.* 20, 467-474; Hele, 2001, The heterotopic tracheal allograft as an animal model of obliterative bronchiolitis. *Respir. Res.*, 2, 169-183; Floege *et al.* 1999, *Am. J. Pathol.*, 154, 169 (animal model of acute glomerulonephritis). Similarly, using various animal models of oncology known in the
10 art, animals treated with siNA molecules of the invention targeting PDGF and/or PDGFr RNA can be evaluated for clinical response (e.g., decreased tumor size/metastasis) and/or decreased levels of Myc RNA or protein.

Example 9: RNAi mediated inhibition of PDGF and/or PDGFr RNA expression

siNA constructs (**Table III**) are tested for efficacy in reducing PDGF and/or PDGFr
15 RNA expression in, for example HASMC, HeLa, or A549 cells. HASMC, HeLa, or A549 cells are plated approximately 24h before transfection in 96-well plates at 5,000-7,500 cells/well, 100 μ l/well, such that at the time of transfection cells are 70-90% confluent. For transfection, annealed siNAs are mixed with the transfection reagent (Lipofectamine 2000, Invitrogen) in a volume of 50 μ l/well and incubated for 20 min. at
20 room temperature. The siNA transfection mixtures are added to cells to give a final siNA concentration of 25 nM in a volume of 150 μ l. Each siNA transfection mixture is added to 3 wells for triplicate siNA treatments. Cells are incubated at 37° for 24h in the continued presence of the siNA transfection mixture. At 24h, RNA is prepared from each well of treated cells. The supernatants with the transfection mixtures are first removed
25 and discarded, then the cells are lysed and RNA prepared from each well. Target gene expression following treatment is evaluated by RT-PCR for the target gene and for a control gene (36B4, an RNA polymerase subunit) for normalization. The triplicate data is averaged and the standard deviations determined for each treatment. Normalized data are graphed and the percent reduction of target mRNA by active siNAs in comparison to their
30 respective inverted control siNAs was determined.

In a non-limiting example a siNA construct comprising ribonucleotides and 3'-terminal dithymidine caps is assayed along with a chemically modified siNA construct comprising 2'-deoxy-2'-fluoro pyrimidine nucleotides and purine ribonucleotides in which the sense strand of the siNA is further modified with 5' and 3'-terminal inverted deoxyabasic caps and the antisense strand comprises a 3'-terminal phosphorothioate internucleotide linkage. These siNA constructs are compared to appropriate matched chemistry inverted controls. In addition, the siNA constructs are also compared to untreated cells, cells transfected with lipid and scrambled siNA constructs, and cells transfected with lipid alone (transfection control).

10 Example 10: Indications

The present body of knowledge in PDGF and PDGFr research indicates the need for methods and compounds that can regulate PDGF and PDGFr gene product expression for research, diagnostic, and therapeutic use. As described herein, the nucleic acid molecules of the present invention can be used to treat leukemias, including acute myelogenous leukemia (AML), chronic myelogenous leukemia (CML), Acute lymphocytic leukemia (ALL), and chronic lymphocytic leukemia; ovarian cancer, breast cancer, cancers of the head and neck, lymphomas, such as mantle cell lymphoma, non-Hodgkin's lymphoma, and Burkitt's lymphoma, adenoma, squamous cell carcinoma, laryngeal carcinoma, multiple myeloma, melanoma, colorectal cancer, prostate cancer, and inflammatory and proliferative diseases such as restenosis, polycystic kidney disease, obliterative bronchiolitis, acute glomerulonephritis, stroke (CVA), and any other diseases or conditions that are related to or will respond to the levels of PDGF and/or PDGFr in a cell or tissue, alone or in combination with other therapies.

The use of radiation treatments and chemotherapeutics such as Gemcytabine and cyclophosphamide are non-limiting examples of chemotherapeutic agents that can be combined with or used in conjunction with the nucleic acid molecules (e.g. siNA molecules) of the instant invention. Those skilled in the art will recognize that other anti-cancer and/or antiproliferative compounds and therapies can be similarly be readily combined with the nucleic acid molecules of the instant invention (e.g. siNA molecules) and are hence within the scope of the instant invention. Such compounds and therapies are well known in the art (see for example *Cancer: Principles and Practice of Oncology*,

Volumes 1 and 2, eds Devita, V.T., Hellman, S., and Rosenberg, S.A., J.B. Lippincott Company, Philadelphia, USA; incorporated herein by reference) and include, without limitations, folates, antifolates, pyrimidine analogs, fluoropyrimidines, purine analogs, adenosine analogs, topoisomerase I inhibitors, anthracyclins, retinoids, antibiotics, anthacyclins, platinum analogs, alkylating agents, nitrosoureas, plant derived compounds such as vinca alkaloids, epipodophyllotoxins, tyrosine kinase inhibitors, taxols, radiation therapy, surgery, nutritional supplements, gene therapy, radiotherapy, for example 3D-CRT, immunotoxin therapy, for example ricin, and monoclonal antibodies. Specific examples of chemotherapeutic compounds that can be combined with or used in conjunction with the nucleic acid molecules of the invention include, but are not limited to, Paclitaxel; Docetaxel; Methotrexate; Doxorubin; Edatrexate; Vinorelbine; Tamoxifen; Leucovorin; 5-fluoro uridine (5-FU); Irinotecan; Cisplatin; Carboplatin; Amsacrine; Cytarabine; Bleomycin; Mitomycin C; Dactinomycin; Mithramycin; Hexamethylmelamine; Dacarbazine; L-asparaginase; Nitrogen mustard; Melphalan, Chlorambucil; Busulfan; Ifosfamide; 4-hydroperoxycyclophosphamide, Thiotepa; Irinotecan (CAMPTOSAR®, CPT-11, Camptothecin-11, Campto) Tamoxifen, Herceptin; IMC C225; ABX-EGF; and combinations thereof. are non-limiting examples of compounds and/or methods that can be combined with or used in conjunction with the nucleic acid molecules (e.g. siNA) of the instant invention. Those skilled in the art will recognize that other drug compounds and therapies can be similarly be readily combined with the nucleic acid molecules of the instant invention (e.g., siNA molecules) are hence within the scope of the instant invention.

Example 11: Diagnostic uses

The siNA molecules of the invention can be used in a variety of diagnostic applications, such as in identifying molecular targets such as RNA in a variety of applications, for example, in clinical, industrial, environmental, agricultural and/or research settings. Such diagnostic use of siNA molecules involves utilizing reconstituted RNAi systems, for example using cellular lysates or partially purified cellular lysates. siNA molecules of this invention can be used as diagnostic tools to examine genetic drift and mutations within diseased cells or to detect the presence of endogenous or exogenous, for example viral, RNA in a cell. The close relationship between siNA activity and the structure of the target RNA allows the detection of mutations in any region of the

molecule, which alters the base-pairing and three-dimensional structure of the target RNA. By using multiple siNA molecules described in this invention, one can map nucleotide changes, which are important to RNA structure and function *in vitro*, as well as in cells and tissues. Cleavage of target RNAs with siNA molecules can be used to
5 inhibit gene expression and define the role (essentially) of specified gene products in the progression of disease or infection. In this manner, other genetic targets can be defined as important mediators of the disease. These experiments will lead to better treatment of the disease progression by affording the possibility of combination therapies (e.g., multiple siNA molecules targeted to different genes, siNA molecules coupled with known small
10 molecule inhibitors, or intermittent treatment with combinations siNA molecules and/or other chemical or biological molecules). Other *in vitro* uses of siNA molecules of this invention are well known in the art, and include detection of the presence of mRNAs associated with a disease, infection, or related condition. Such RNA is detected by determining the presence of a cleavage product after treatment with a siNA using
15 standard methodologies, for example, fluorescence resonance emission transfer (FRET).

In a specific example, siNA molecules that cleave only wild-type or mutant forms of the target RNA are used for the assay. The first siNA molecules (*i.e.*, those that cleave only wild-type forms of target RNA) are used to identify wild-type RNA present in the sample and the second siNA molecules (*i.e.*, those that cleave only mutant forms of target
20 RNA) are used to identify mutant RNA in the sample. As reaction controls, synthetic substrates of both wild-type and mutant RNA are cleaved by both siNA molecules to demonstrate the relative siNA efficiencies in the reactions and the absence of cleavage of the "non-targeted" RNA species. The cleavage products from the synthetic substrates also serve to generate size markers for the analysis of wild-type and mutant RNAs in the
25 sample population. Thus, each analysis requires two siNA molecules, two substrates and one unknown sample which is combined into six reactions. The presence of cleavage products is determined using an RNase protection assay so that full-length and cleavage fragments of each RNA can be analyzed in one lane of a polyacrylamide gel. It is not absolutely required to quantify the results to gain insight into the expression of mutant
30 RNAs and putative risk of the desired phenotypic changes in target cells. The expression of mRNA whose protein product is implicated in the development of the phenotype (*i.e.*, disease related or infection related) is adequate to establish risk. If probes of comparable

specific activity are used for both transcripts, then a qualitative comparison of RNA levels is adequate and decreases the cost of the initial diagnosis. Higher mutant form to wild-type ratios are correlated with higher risk whether RNA levels are compared qualitatively or quantitatively.

5 All patents and publications mentioned in the specification are indicative of the levels of skill of those skilled in the art to which the invention pertains. All references cited in this disclosure are incorporated by reference to the same extent as if each reference had been incorporated by reference in its entirety individually.

10 One skilled in the art would readily appreciate that the present invention is well adapted to carry out the objects and obtain the ends and advantages mentioned, as well as those inherent therein. The methods and compositions described herein as presently representative of preferred embodiments are exemplary and are not intended as limitations on the scope of the invention. Changes therein and other uses will occur to those skilled in the art, which are encompassed within the spirit of the invention, are
15 defined by the scope of the claims.

It will be readily apparent to one skilled in the art that varying substitutions and modifications can be made to the invention disclosed herein without departing from the scope and spirit of the invention. Thus, such additional embodiments are within the scope of the present invention and the following claims. The present invention teaches one
20 skilled in the art to test various combinations and/or substitutions of chemical modifications described herein toward generating nucleic acid constructs with improved activity for mediating RNAi activity. Such improved activity can comprise improved stability, improved bioavailability, and/or improved activation of cellular responses mediating RNAi. Therefore, the specific embodiments described herein are not limiting
25 and one skilled in the art can readily appreciate that specific combinations of the modifications described herein can be tested without undue experimentation toward identifying siNA molecules with improved RNAi activity.

The invention illustratively described herein suitably can be practiced in the absence of any element or elements, limitation or limitations that are not specifically
30 disclosed herein. Thus, for example, in each instance herein any of the terms "comprising", "consisting essentially of", and "consisting of" may be replaced with either

of the other two terms. The terms and expressions which have been employed are used as terms of description and not of limitation, and there is no intention that in the use of such terms and expressions of excluding any equivalents of the features shown and described or portions thereof, but it is recognized that various modifications are possible within the scope of the invention claimed. Thus, it should be understood that although the present invention has been specifically disclosed by preferred embodiments, optional features, modification and variation of the concepts herein disclosed may be resorted to by those skilled in the art, and that such modifications and variations are considered to be within the scope of this invention as defined by the description and the appended claims.

10 In addition, where features or aspects of the invention are described in terms of Markush groups or other grouping of alternatives, those skilled in the art will recognize that the invention is also thereby described in terms of any individual member or subgroup of members of the Markush group or other group.

Table I: PDGFr and PDGF Accession Numbers

NM_002609	Homo sapiens platelet-derived growth factor receptor, beta polypeptide (PDGFRB), mRNA
gi 15451788 ref NM_002609.2 [15451788]	
NM_006206	Homo sapiens platelet-derived growth factor receptor, alpha polypeptide (PDGFRA), mRNA
gi 15451787 ref NM_006206.2 [15451787]	
1: BD166138	Platelet-derived growth factor receptors
gi 27871950 dbj BD166138.1 pat JP 2002186490 3[27871950]	
BD166137	Platelet-derived growth factor receptors
gi 27871949 dbj BD166137.1 pat JP 2002186490 2[27871949]	
BD166136	Platelet-derived growth factor receptors
gi 27871948 dbj BD166136.1 pat JP 2002186490 1[27871948]	
NM_033016	Homo sapiens platelet-derived growth factor beta polypeptide (simian sarcoma viral (v-sis) oncogene homolog) (PDGFB), transcript variant 2, mRNA
gi 15451785 ref NM_033016.1 [15451785]	

NM_002608
Homo sapiens platelet-derived growth factor beta polypeptide (simian sarcoma viral (v-sis) oncogene homolog) (PDGFB), transcript variant 1, mRNA
gi|4505680|ref|NM_002608.1|[4505680]

M59423
Human platelet-derived growth factor A-chain (PDGF) gene, 5' end and promoter region
gi|189877|gb|M59423.1|HUMPGDF[189877]

Y14326
Homo sapiens platelet derived growth factor, B-chain 5'UTR
gi|2832416|emb|Y14326.1|HSPDGFBC[2832416]

X83705
H.sapiens mRNA for c-sis proto-oncogene
gi|951023|emb|X83705.1|HSRNASIS[951023]

X00562
Human proto-oncogene c-sis fragment for PDGF B chain precursor (platelet-derived growth factor)
gi|36477|emb|X00562.1|HSSISB5[36477]

X00561
Human proto-oncogene c-sis fragment for PDGF B chain precursor (platelet-derived growth factor)
gi|36474|emb|X00561.1|HSSISB4[36474]

X00560
Human proto-oncogene c-sis fragment for PDGF B chain precursor (platelet-derived growth factor)
gi|36472|emb|X00560.1|HSSISB3[36472]

X00559
Human proto-oncogene c-sis fragment for PDGF B chain precursor (platelet-derived growth factor)
gi|36470|emb|X00559.1|HSSISB2[36470]

X00556
Human proto-oncogene c-sis fragment for PDGF B chain precursor (platelet-derived growth factor)
gi|36468|emb|X00556.1|HSSISB1[36468]

X02811
Human mRNA for platelet-derived growth factor B chain (PDGF-B)
gi|35371|emb|X02811.1|HSPDGF B[35371]

X03795
Human mRNA for platelet derived growth factor A-chain (PDGF-A)
gi|35365|emb|X03795.1|HSPDGFAR[35365]

X06374
Human mRNA for platelet-derived growth factor PDGF-A
gi|35363|emb|X06374.1|HSPDGF A[35363]

AF417590
Homo sapiens platelet-derived growth factor A chain (PDGFA) gene, exon 1 and

partial sequence
gi|16033732|gb|AF417590.1|AF417590[16033732]

NM_006206
Homo sapiens platelet-derived growth factor receptor, alpha polypeptide
(PDGFRA), mRNA
gi|15451787|ref|NM_006206.2|[15451787]

AF244813
Homo sapiens platelet-derived growth factor C mRNA, complete cds
gi|8886883|gb|AF244813.1|AF244813[8886883]

NM_002607
Homo sapiens platelet-derived growth factor alpha polypeptide (PDGFA),
transcript variant 1, mRNA
gi|15208657|ref|NM_002607.2|[15208657]

Table II: PDGFR siNA and Target Sequences

PDGFRB NM_002609.2									
Pos	Seq	Seq ID	UPos	Upper seq	Seq ID	LPos	Lower seq	Seq ID	
3	CCCCUCAGCCCUUGCUGCCC	1	3	CCCCUCAGCCCUUGCUGCCC	1	25	GGGACAGAGCCGCGGAGGG	312	
21	CAGCAGAGCCCUUGCUGC	2	21	CAGCAGAGCCCUUGCUGC	2	43	CGAGCAGAGCCCUUGCUG	313	
39	GCCUCGCCCCAACGCAGACA	3	39	GCCUCGCCCCAACGCAGACA	3	61	UGUCUGCGUUGGCGAGGGC	314	
57	AGCCAGACCCAGGGCGGCC	4	57	AGCCAGACCCAGGGCGGCC	4	79	GGCCGCCCUUGGUCUGGCU	315	
75	CCUCUCGGCGGCUCUCUC	5	75	CCUCUCGGCGGCUCUCUC	5	97	GAGCAGAGCCGCGCAGAGGG	316	
93	CCUCCCGAAGGAUGCUUGG	6	93	CCUCCCGAAGGAUGCUUGG	6	115	CCAAGCAUCCUUCGGGAGG	317	
111	GGGAGUGAGGCGAAGCUGG	7	111	GGGAGUGAGGCGAAGCUGG	7	133	CCAGCUUCGCCUCACUCCC	318	
129	GGCGCUCCUCUCCCCUACA	8	129	GGCGCUCCUCUCCCCUACA	8	151	UGUAGGGGAGAGGAGCGCC	319	
147	AGCAGCCCCCUUCCUCCAU	9	147	AGCAGCCCCCUUCCUCCAU	9	169	AUGGAGGAAGGGGGCUGCU	320	
165	UCCUCUCGUUUCUCCUGAGC	10	165	UCCUCUCGUUUCUCCUGAGC	10	187	GCUCAGGAGAACAGAGGGA	321	
183	CCUUCAGGAGCCUGCACCA	11	183	CCUUCAGGAGCCUGCACCA	11	205	UGGUCAGGCUCCUGAAGG	322	
201	AGUCCUGCCUGUCCUUCUA	12	201	AGUCCUGCCUGUCCUUCUA	12	223	UAGAAGGACAGGACGAGCU	323	
219	ACUCAGCUGUUAACCCACUC	13	219	ACUCAGCUGUUAACCCACUC	13	241	GAGUGGGUAACAGCUGAGU	324	
237	CUGGGACCAGCAGUCUUC	14	237	CUGGGACCAGCAGUCUUC	14	259	GAAAGACUCUGGUGUCCAG	325	
255	CUGAUAACUGGGAGAGGGC	15	255	CUGAUAACUGGGAGAGGGC	15	277	GCCUCUCCAGUUAUCAG	326	
273	CAGUAAGGAGGACUCCUG	16	273	CAGUAAGGAGGACUCCUG	16	295	CAGGAAGUCCUCCUUCUG	327	
291	GGAGGGGUGACUUGCCAG	17	291	GGAGGGGUGACUUGCCAG	17	313	CUGGACAGUACCCUCCUCC	328	
309	GAGCCUGGAACUGUGCCCA	18	309	GAGCCUGGAACUGUGCCCA	18	331	UGGGCACAGUCCAGGCUC	329	
327	ACACCAGAAAGCCAUACAGCA	19	327	ACACCAGAAAGCCAUACAGCA	19	349	UGCUGAUGGCUUCUGGUGU	330	
345	AGCAAGGACACCAUGCGGC	20	345	AGCAAGGACACCAUGCGGC	20	367	GCCGCAUGGUGUCCUUGCU	331	
363	CUUCCGGGUGCGAUGCCAG	21	363	CUUCCGGGUGCGAUGCCAG	21	385	CUGGCAUCGACCCCGGAAG	332	
381	GCUCUGGCCCUCAAAGGCG	22	381	GCUCUGGCCCUCAAAGGCG	22	403	CGCCUUUGAGGGCCAGAGC	333	
399	GAGCUGCUGUUGCUGUCUC	23	399	GAGCUGCUGUUGCUGUCUC	23	421	GAGACAGCAACAGCAGCUC	334	
417	CUCCUGUUAUUCUGGAAC	24	417	CUCCUGUUAUUCUGGAAC	24	439	GUUCCAGAAGUAACAGGAG	335	
435	CCACAGAUCUCUCAGGGCC	25	435	CCACAGAUCUCUCAGGGCC	25	457	GGCCUUGAGAGAUUCUGUGG	336	
453	CUGGUCGUCACACCCCGG	26	453	CUGGUCGUCACACCCCGG	26	475	CCGGGGUGUGACGACCAG	337	
471	GGCCAGAGCUUUGCUCA	27	471	GGCCAGAGCUUUGCUCA	27	493	UGAGGACAAGCUCUGGCC	338	
489	AUGUCUCCAGCACCUUCG	28	489	AUGUCUCCAGCACCUUCG	28	511	CGAAGGUGCUGGAGACAUU	339	
507	GUUCUGACCUGCUGGGU	29	507	GUUCUGACCUGCUGGGU	29	529	AACCCGAGCAGGUCAGAAC	340	
525	UCAGCUCCGGUGUGUGG	30	525	UCAGCUCCGGUGUGUGG	30	547	CCCACACCACCGGAGCUGA	341	
543	GAACGGAUGUCCAGGAGC	31	543	GAACGGAUGUCCAGGAGC	31	565	GCUCCUGGACAUCCGCUUC	342	

561	CCCCACAGGAAUUGGCCA	32	561	CCCCACAGGAAUUGGCCA	32	583	UGGCCAUUUUCCUGUGGGGG	343
579	AAGGCCACAGGAUUGGCACCU	33	579	AAGGCCACAGGAUUGGCACCU	33	601	AGGUGCCAUUCCUGGGCCUU	344
597	UUCUCCAGCGUGCUCACAC	34	597	UUCUCCAGCGUGCUCACAC	34	619	GUGUGAGCACGCGUGGAGAA	345
615	CUGACCAACCUACUGGGC	35	615	CUGACCAACCUACUGGGC	35	637	GGCCAGUGAGGUUGGUCAG	346
633	CUAGACACGGGAGAAUACU	36	633	CUAGACACGGGAGAAUACU	36	655	AGUUAUUCUCCCGUGUCUAG	347
651	UUUUGCACCCACAAUAGACU	37	651	UUUUGCACCCACAAUAGACU	37	673	AGUCAUUGUGGGUGCAAAA	348
669	UCCCGUGGACUUGGAGACCG	38	669	UCCCGUGGACUUGGAGACCG	38	691	CGGUCUCCAGUCCACGGGA	349
687	GAUGAGCGGAAACGGCUCU	39	687	GAUGAGCGGAAACGGCUCU	39	709	AGAGCCGUUUCGCGUCAUC	350
705	UACAUCUUUGUGCCAGAU	40	705	UACAUCUUUGUGCCAGAU	40	727	GAUCUGGCACAAAGAUGUA	351
723	CCCACGUGGGCUUCCUCC	41	723	CCCACGUGGGCUUCCUCC	41	745	GGAGGAAGCCACCGGUGGG	352
741	CCUAAUGAUGCCGAGGAAC	42	741	CCUAAUGAUGCCGAGGAAC	42	763	GUUCCUGGGCAUCAUAGG	353
759	CUAUUCAUCUUUCACGG	43	759	CUAUUCAUCUUUCACGG	43	781	CCGUGAGAAAGAUAGAAUAG	354
777	GAAUUAACUGAGAUACCA	44	777	GAAUUAACUGAGAUACCA	44	799	UGGUGAUCUCAGUUAUUUC	355
795	AUCCAUGCCGAGUAACAG	45	795	AUCCAUGCCGAGUAACAG	45	817	CUGUUAUCUGGGCAUGGAU	356
813	GACCCACAGCUGGUGGUGA	46	813	GACCCACAGCUGGUGGUGA	46	835	UCACCACGACGUGUGGUC	357
831	ACACUGCACGAGAAGAAAG	47	831	ACACUGCACGAGAAGAAAG	47	853	CUUUCUUCUGGUCAGUGU	358
849	GGGACGUGUACUGCCUG	48	849	GGGACGUGUACUGCCUG	48	871	CAGGCAGUGCAACGUCGCC	359
867	GUCCCUUAUGAUCACCAAC	49	867	GUCCCUUAUGAUCACCAAC	49	889	GUUGGUGAUCUAAGGGGAC	360
885	CGUGGCUUUUCUGGUAUCU	50	885	CGUGGCUUUUCUGGUAUCU	50	907	AGUAACCAAGAAAGCCACG	361
903	UUUGAGGACAGAGCUACA	51	903	UUUGAGGACAGAGCUACA	51	925	UGUAGCUUCUGUCCUCAAA	362
921	AUCUGCAAAACCAACCAUUG	52	921	AUCUGCAAAACCAACCAUUG	52	943	CAUUGGUGGUUUUUGCAGAU	363
939	GGGACAGGGAGGUGGAUU	53	939	GGGACAGGGAGGUGGAUU	53	961	AAUCCACUCCUUGUCCCC	364
957	UCUGAUGCCUACUAUGUCU	54	957	UCUGAUGCCUACUAUGUCU	54	979	AGACAUAGUAGGCAUCAGA	365
975	UACAGACUCCAGGUGUCAU	55	975	UACAGACUCCAGGUGUCAU	55	997	AUGACACUUGGAGUCUGUA	366
993	UCCAUCACGUCUCUGUGA	56	993	UCCAUCACGUCUCUGUGA	56	1015	UCACAGAGACGUUGAUGGA	367
1011	AACGCAGUGCAGACUGUGG	57	1011	AACGCAGUGCAGACUGUGG	57	1033	CCACAGUCUGCACUGCGUU	368
1029	GUCCGCCAGGGUGAGAACA	58	1029	GUCCGCCAGGGUGAGAACA	58	1051	UGUUCACCCUGGCGGAC	369
1047	AUCACCCUACUUGCAUUG	59	1047	AUCACCCUACUUGCAUUG	59	1069	CAUUGCACAUGAGGGUGAU	370
1065	GUGAUCGGGAAUAGAGGUGG	60	1065	GUGAUCGGGAAUAGAGGUGG	60	1087	CCACCUCAUUCGCCGAUCAC	371
1083	GUCAACUUCGAGUGGACAU	61	1083	GUCAACUUCGAGUGGACAU	61	1105	AUGUCCACUCGAAGUUGAC	372
1101	UACCCCGCAAAGAAAGUG	62	1101	UACCCCGCAAAGAAAGUG	62	1123	CACUUCUUUUGCGGGGUA	373
1119	GGGCGGUGGUGGAGCCCGG	63	1119	GGGCGGUGGUGGAGCCCGG	63	1141	CCGGUCCACACAGCCGCC	374
1137	GUGACUGACUUCUUCUUGG	64	1137	GUGACUGACUUCUUCUUGG	64	1159	CCAAGAGGAAGUCAGUCAC	375
1155	GAUAGCCUUAACCAUCC	65	1155	GAUAGCCUUAACCAUCC	65	1177	GGAUGUGGUAAGGCAUUC	376
1173	CGCUCCAUCUCCGACAUCC	66	1173	CGCUCCAUCUCCGACAUCC	66	1195	GGAUGUGCAGGAUGGAGCG	377
1191	CCCAGUGCCGAGUUAAGAAG	67	1191	CCCAGUGCCGAGUUAAGAAG	67	1213	CUUCUAACUCCGACUGGG	378
1209	GACUCGGGACCUACACCU	68	1209	GACUCGGGACCUACACCU	68	1231	AGGUGUAGGUCCCCGAGUC	379

1227	UGAAUGUGACGGAGAGUG	69	1227	UGAAUGUGACGGAGAGUG	69	1249	CACUUCGUCACAUUGCA	380
1245	GUGAAUGACCAUCAGGAUG	70	1245	GUGAAUGACCAUCAGGAUG	70	1267	CAUCCUGAUGGUCUUCAC	381
1263	GAAAAGGCCAUCAACAUA	71	1263	GAAAAGGCCAUCAACAUA	71	1285	UGAUGUUGAUGGCCUUCU	382
1281	ACCGUGGUUGAGAGCGGCU	72	1281	ACCGUGGUUGAGAGCGGCU	72	1303	AGCCGCUUCACACACGGU	383
1299	UACGUGCGGUUCCUGGGAG	73	1299	UACGUGCGGUUCCUGGGAG	73	1321	CUCCAGGAGCCGACGUA	384
1317	GAGGUGGGCACACUACAAU	74	1317	GAGGUGGGCACACUACAAU	74	1339	AUUGAUGUGCCACCUUC	385
1335	UUUGCUGAGCUGCAUCGGA	75	1335	UUUGCUGAGCUGCAUCGGA	75	1357	UCCGAUGCAGCUCAGCAA	386
1353	AGCCGGACACUGCAGGUAG	76	1353	AGCCGGACACUGCAGGUAG	76	1375	CUACUGCAGUGUCCGGCU	387
1371	GUGUUCGAGGCCUACCCAC	77	1371	GUGUUCGAGGCCUACCCAC	77	1393	GUGGUAGGCCUUCGAACAC	388
1389	CCGCCACUGUCCUGUGGU	78	1389	CCGCCACUGUCCUGUGGU	78	1411	ACCACAGACAGUGGGCGG	389
1407	UUCAAAGACAACCGCACCC	79	1407	UUCAAAGACAACCGCACCC	79	1429	GGGUGCGGUUGUCUUGAA	390
1425	CUGGGCAGUCCAGCGCUG	80	1425	CUGGGCAGUCCAGCGCUG	80	1447	CAGCGCUGGAGUCGCCAG	391
1443	GGCGAAUUCGCCUGUCCA	81	1443	GGCGAAUUCGCCUGUCCA	81	1465	UGGACAGGGCGAUUUCGCC	392
1461	ACGCGCAACGUGUCGGAGA	82	1461	ACGCGCAACGUGUCGGAGA	82	1483	UCUCCGACACGUGCGCGU	393
1479	ACCGGUAUGUGUCAGAGC	83	1479	ACCGGUAUGUGUCAGAGC	83	1501	GCUCUGACACAUACCGGCU	394
1497	CUGACACUGGUUCGCGUGA	84	1497	CUGACACUGGUUCGCGUGA	84	1519	UCACGCGAACCAAGUGUCAG	395
1515	AAGGUGGCAGAGGCGUGCC	85	1515	AAGGUGGCAGAGGCGUGCC	85	1537	GGCCAGCCUCUGCCACCUU	396
1533	CACUACACCAUGCGGGCCU	86	1533	CACUACACCAUGCGGGCCU	86	1555	AGGCCGCAUGGUGUAGUG	397
1551	UUCCAUGAGGAUGCUGAGG	87	1551	UUCCAUGAGGAUGCUGAGG	87	1573	CCUCAGCAUCCUCUAGGAA	398
1569	GUCCAGCUCUCCUUCACGC	88	1569	GUCCAGCUCUCCUUCACGC	88	1591	GCUGGAAGGAGAGCUGGAC	399
1587	CUACAGAUCAAUGUCCUG	89	1587	CUACAGAUCAAUGUCCUG	89	1609	CAGGGACAUUGAUUCUUGAG	400
1605	GUCCGAGUGCUGGAGCUAA	90	1605	GUCCGAGUGCUGGAGCUAA	90	1627	UUAGCUCACGACUCGGAC	401
1623	AGUGAGAGCCACCCUGACA	91	1623	AGUGAGAGCCACCCUGACA	91	1645	UGUCAGGGUGGCUCUCACU	402
1641	AGUGGGGAACAGACAGUCC	92	1641	AGUGGGGAACAGACAGUCC	92	1663	GGACUGUCUUGUCCCCACU	403
1659	CGCUGUCUGUGCCGGGGCA	93	1659	CGCUGUCUGUGCCGGGGCA	93	1681	UGCCCCGGCCACGACAGCG	404
1677	AUGCCCCAGCCGAACAUA	94	1677	AUGCCCCAGCCGAACAUA	94	1699	UGAUGUUCGGCUGGGGCAU	405
1695	AUCUGGUCUGCCUGCAGAG	95	1695	AUCUGGUCUGCCUGCAGAG	95	1717	CUCUGCAGGCAGACCAGAU	406
1713	GACCUCAAAAGGUGUCCAC	96	1713	GACCUCAAAAGGUGUCCAC	96	1735	GUGGACACCUUUUGAGGUC	407
1731	CGUGAGCUGCCGCCACGC	97	1731	CGUGAGCUGCCGCCACGC	97	1753	GCGUGGGCGGCAGCUCACG	408
1749	CUGCUGGGGAACAGUCCG	98	1749	CUGCUGGGGAACAGUCCG	98	1771	CGGAACUGUUCGCCAGCAG	409
1767	GAAGAGGAGAGCCAGCUGG	99	1767	GAAGAGGAGAGCCAGCUGG	99	1789	CCAGCUGGCUCUCCUCUUC	410
1785	GAGACUACGUGACGUACU	100	1785	GAGACUACGUGACGUACU	100	1807	AGUACGUCACGUUAGUCUC	411
1803	UGGAGGAGGAGCAGGAGU	101	1803	UGGAGGAGGAGCAGGAGU	101	1825	ACUCCUGCUCUCCUCCCA	412
1821	UUUGAGGUGGUGAGCACAC	102	1821	UUUGAGGUGGUGAGCACAC	102	1843	GUGUGCUCACCCACCUCAA	413
1839	CUGCGUCUGCAGCACGUGG	103	1839	CUGCGUCUGCAGCACGUGG	103	1861	CCACGUGCUGCAGACGCGAG	414
1857	GAUCGGCCACUGUCGGUGC	104	1857	GAUCGGCCACUGUCGGUGC	104	1879	GCACCGACAGUGGCCGAUC	415
1875	CGCUGCACGCUGCGCAACG	105	1875	CGCUGCACGCUGCGCAACG	105	1897	CGUUGCGCAGCGUGCAGCG	416

1893	GCUUGGGCCAGGACACGC	106	1893	GCUUGGGCCAGGACACGC	106	1915	GCGUGUCCUUGGCCACAGC	417
1911	CAGGAGGUCAUCGUGGUGC	107	1911	CAGGAGGUCAUCGUGGUGC	107	1933	GCACCACGAUGACCUCCUG	418
1929	CCACACUCCUUGCCCUUUA	108	1929	CCACACUCCUUGCCCUUUA	108	1951	UAAAGGGCAAGGAGUGUG	419
1947	AAGGUGGUGGUGAUCUCAG	109	1947	AAGGUGGUGGUGAUCUCAG	109	1969	CUGAGAUACACACACCUU	420
1965	GCAUCCUGGCCUGGUGG	110	1965	GCAUCCUGGCCUGGUGG	110	1987	CCACCAGGGCCAGGAUGGC	421
1983	GUGCUCACCAUCAUCUCC	111	1983	GUGCUCACCAUCAUCUCC	111	2005	GGGAGAUAGGUGAGCAC	422
2001	CUUAUCAUCCUCAUAGC	112	2001	CUUAUCAUCCUCAUAGC	112	2023	GCAUGAUGAGGAUGAUAG	423
2019	CUUUGGCAGAAAGCCAC	113	2019	CUUUGGCAGAAAGCCAC	113	2041	GUGGCUUCUUCUGCCAAAG	424
2037	CGUACGAGAUCCGAUGGA	114	2037	CGUACGAGAUCCGAUGGA	114	2059	UCCAUCCGAUCUCGUAACG	425
2055	AAGGUAUUGAGUCUGUGA	115	2055	AAGGUAUUGAGUCUGUGA	115	2077	UCACAGACUAAUACACCUU	426
2073	AGCUCUGACGGCCAUAGU	116	2073	AGCUCUGACGGCCAUAGU	116	2095	ACUCAUGGCCGUCAGAGCU	427
2091	UACAUCUACGUGGACCCCA	117	2091	UACAUCUACGUGGACCCCA	117	2113	UGGGGUCCACGUAGAUGUA	428
2109	AUGCAGCUGCCCUAUGACU	118	2109	AUGCAGCUGCCCUAUGACU	118	2131	AGUCAUAGGGCAGCUGCAU	429
2127	UCCACGUGGGAGCUGCCGC	119	2127	UCCACGUGGGAGCUGCCGC	119	2149	GGGGCAGUCCACCGUGGA	430
2145	CGGGACCAAGCUUGUGCUGG	120	2145	CGGGACCAAGCUUGUGCUGG	120	2167	CCAGACAAGCUGGUCGCG	431
2163	GGACGCACCCUCGGCUCUG	121	2163	GGACGCACCCUCGGCUCUG	121	2185	CAGAGCCAGGUGGCGUCC	432
2181	GGGGCCUUGGGCAGGUGG	122	2181	GGGGCCUUGGGCAGGUGG	122	2203	CCACCUGCCCAAAGGCCCC	433
2199	GUGGAGGCCACGGCUCUAG	123	2199	GUGGAGGCCACGGCUCUAG	123	2221	CAUGAGCCGUGGGCCUCCAC	434
2217	GGCCUGAGCCAUUCUCAGG	124	2217	GGCCUGAGCCAUUCUCAGG	124	2239	CCUGAGAAUGGUCACAGGC	435
2235	GCCACGAUGAAAGUGGCCG	125	2235	GCCACGAUGAAAGUGGCCG	125	2257	CGGCCACUUUCAUGUGGC	436
2253	GUCAAGAUGCUIAAAUCCA	126	2253	GUCAAGAUGCUIAAAUCCA	126	2275	UGGAUUUAAGCAUCUUGAC	437
2271	ACAGCCCGCAGCAGUGAGA	127	2271	ACAGCCCGCAGCAGUGAGA	127	2293	UCUCACUGCUGCGGGCUGU	438
2289	AAGCAAGCCCUUAUGUCGG	128	2289	AAGCAAGCCCUUAUGUCGG	128	2311	CCGACAUAAAGGGCUUGCUU	439
2307	GAGCUGAAGAUCAUGAGUC	129	2307	GAGCUGAAGAUCAUGAGUC	129	2329	GACUCAUGAUUUCAGCUC	440
2325	CACCUUGGGCCCCACCUGA	130	2325	CACCUUGGGCCCCACCUGA	130	2347	UCAGGUGGGGCCCAAGGUG	441
2343	AACGUGGUCAACCUUUGG	131	2343	AACGUGGUCAACCUUUGG	131	2365	CCAACAGUUGACCACGUU	442
2361	GGGGCCUGCACCAAGGAG	132	2361	GGGGCCUGCACCAAGGAG	132	2383	CUCCUUUGGUGCAGGCCCC	443
2379	GGACCAUCUAUAUCAUCA	133	2379	GGACCAUCUAUAUCAUCA	133	2401	UGAUGAUUAAGAUGGGUCC	444
2397	ACUGAGUACUGCCGCUACG	134	2397	ACUGAGUACUGCCGCUACG	134	2419	CGUAGCGGCAGUACUCAGU	445
2415	GGAGACCUGGUGGACUACC	135	2415	GGAGACCUGGUGGACUACC	135	2437	GGUAGUCCACCAAGGUCUC	446
2433	CUGACCCGCAACAACACA	136	2433	CUGACCCGCAACAACACA	136	2455	UGUUGUUUGUUGCGGUGCAG	447
2451	ACCUUCCUGCAGCACCCACU	137	2451	ACCUUCCUGCAGCACCCACU	137	2473	AGUUGGUCUGCAGGAAGGU	448
2469	UCCGACAAGCGCCGCCCGC	138	2469	UCCGACAAGCGCCGCCCGC	138	2491	GCGGGCGCGCUUGUCGGA	449
2487	CCCAGCGCGGAGCUCUACA	139	2487	CCCAGCGCGGAGCUCUACA	139	2509	UGUAGAGCUCCGCGCUGGG	450
2505	AGCAUUGCUCUGCCCGUUG	140	2505	AGCAUUGCUCUGCCCGUUG	140	2527	CAACGGGCAGAGCAUUGCU	451
2523	GGGCUCCCCCUGCCAGCC	141	2523	GGGCUCCCCCUGCCAGCC	141	2545	GGCUGGGCAGGGGAGGCC	452
2541	CAUGUGUCCUUGACCGGGG	142	2541	CAUGUGUCCUUGACCGGGG	142	2563	CCCCGGUCAAGGACACAUG	453

2559	GAGAGCAGCGGUGGCUACA	143	2559	GAGAGCAGCGGUGGCUACA	143	2581	UGUAGCCACCGUCGUCUC	454
2577	AUGGACAUGAGCAAGGACG	144	2577	AUGGACAUGAGCAAGGACG	144	2599	CGUCCUUGCUCAUGUCCAU	455
2595	GAGUCGGUGGACUAUGUGC	145	2595	GAGUCGGUGGACUAUGUGC	145	2617	GCACUAUGUCCACCGACUC	456
2613	CCCAUGCUGGACAUAAAAG	146	2613	CCCAUGCUGGACAUAAAAG	146	2635	CUUUAUGUCCACGAGUGG	457
2631	GGAGACGUCAAAUAUAGCAG	147	2631	GGAGACGUCAAAUAUAGCAG	147	2653	CUGCAUAUUUAGACGUCUC	458
2649	GACAUCGAGUCCUCCAAUCU	148	2649	GACAUCGAGUCCUCCAAUCU	148	2671	AGUUGGAGGACUGGAUGUC	459
2667	UACAUGGCCCCUUAACGAUA	149	2667	UACAUGGCCCCUUAACGAUA	149	2689	UAUCGUAAGGGGCCCAUGUA	460
2685	AACUACGUUCCUUCUGCCC	150	2685	AACUACGUUCCUUCUGCCC	150	2707	GGGCAGAGGGAAACGUAGUU	461
2703	CCUGAGAGGACCUUGCCGAG	151	2703	CCUGAGAGGACCUUGCCGAG	151	2725	CUCGGCAGGUCCUUCACAGG	462
2721	GCAACUUUGAUAACGAGU	152	2721	GCAACUUUGAUAACGAGU	152	2743	ACUCGUUGAUAACAAAGUUGC	463
2739	UCUCCAGUGCUAAGCUACA	153	2739	UCUCCAGUGCUAAGCUACA	153	2761	UGUAGCUUAGCACUUGGAGA	464
2757	AUGGACCUCUGGGGCUUCA	154	2757	AUGGACCUCUGGGGCUUCA	154	2779	UGAAGCCACGAGGUCCAU	465
2775	AGCUACCAGGUGGCCAAUG	155	2775	AGCUACCAGGUGGCCAAUG	155	2797	CAUUGGCCACCUUGUAGCU	466
2793	GGCAUGGAGUUUCUGGCCU	156	2793	GGCAUGGAGUUUCUGGCCU	156	2815	AGGCCAGAAACUCCAUGCC	467
2811	UCCAAGAACUGCGUCCACA	157	2811	UCCAAGAACUGCGUCCACA	157	2833	UGUGGACGAGUUUCUUGGA	468
2829	AGAGACCUGGGGCUAGGA	158	2829	AGAGACCUGGGGCUAGGA	158	2851	UCCUAGCCGCCAGGUCUCU	469
2847	AACGUGCUCAUCUGUGAAG	159	2847	AACGUGCUCAUCUGUGAAG	159	2869	CUUCACAGAUAGACACGUU	470
2865	GGCAAGCUGGCUAAGAUUCU	160	2865	GGCAAGCUGGCUAAGAUUCU	160	2887	AGAUCUUAGCACGCUUGCC	471
2883	UGUGACUUUGCCUGGCCUC	161	2883	UGUGACUUUGCCUGGCCUC	161	2905	GAGCCAGGCCAAAGUACACA	472
2901	CGAGACAUCAUUGCGGACU	162	2901	CGAGACAUCAUUGCGGACU	162	2923	AGUCCCGCAUGAUGUCUCG	473
2919	UCGAAUUACAUCUCCAAAG	163	2919	UCGAAUUACAUCUCCAAAG	163	2941	CUUUGGAGAUUAUUUCGA	474
2937	GGCAGCACCUUUUUGCCUU	164	2937	GGCAGCACCUUUUUGCCUU	164	2959	AAGGCAAAAGGUGGUGCC	475
2955	UUAAGUGGAUGGCUCCGG	165	2955	UUAAGUGGAUGGCUCCGG	165	2977	CCGGAGCCAUCCACUUAUA	476
2973	GAGAGCAUCUUAACAGCC	166	2973	GAGAGCAUCUUAACAGCC	166	2995	GGCUGUUGAAGAUUCUCUC	477
2991	CUCUACACCAACCCUGAGCG	167	2991	CUCUACACCAACCCUGAGCG	167	3013	CGCUCAGGGUGGUGUAGAG	478
3009	GACGUGUGGUCUUCGGGA	168	3009	GACGUGUGGUCUUCGGGA	168	3031	UCCGGAAGGACACACGUC	479
3027	AUCCUGCUCUGGGAGAUUCU	169	3027	AUCCUGCUCUGGGAGAUUCU	169	3049	AGAUCUCCAGAGCAGGAU	480
3045	UUCACCUUGGGUGGCACCC	170	3045	UUCACCUUGGGUGGCACCC	170	3067	GGGUGCCACCCAAAGGUGAA	481
3063	CCUUAACCCAGAGCUGCCCA	171	3063	CCUUAACCCAGAGCUGCCCA	171	3085	UGGGCAGCUCUGGUAAGG	482
3081	AUGAACGAGCAGUUAUACA	172	3081	AUGAACGAGCAGUUAUACA	172	3103	UGUAGAACUUGCUCGUUAU	483
3099	AAUGCCAUAACAGGGGUU	173	3099	AAUGCCAUAACAGGGGUU	173	3121	AACCCCGUUAUGAUGGCAU	484
3117	UACCGCAUGGCCACGCCUG	174	3117	UACCGCAUGGCCACGCCUG	174	3139	CAGGUGGGCCCAUGCGGUA	485
3135	GCCCAUGCCUCCGACGAGA	175	3135	GCCCAUGCCUCCGACGAGA	175	3157	UCUGCUGGAGGCAUGGGC	486
3153	AUCUAUGAGAUCAUGCAGA	176	3153	AUCUAUGAGAUCAUGCAGA	176	3175	UCUGCAUGAUCUUAUAGAU	487
3171	AAGUGCUGGGAAGAGAAGU	177	3171	AAGUGCUGGGAAGAGAAGU	177	3193	ACUUCUCUCCAGCACUU	488
3189	UUUGAGAUUCGGCCCCCUU	178	3189	UUUGAGAUUCGGCCCCCUU	178	3211	AGGGGGGCCGAAUCUCAAA	489
3207	UUCUCCAGCUGGUGCUGC	179	3207	UUCUCCAGCUGGUGCUGC	179	3229	GCAGCACCGCUGGGAGAA	490

3225	CUUCUCGAGAGACUGUUGG	180	3225	CUUCUCGAGAGACUGUUGG	180	3247	CCAACAGUCUCGAGAAAG	491
3243	GGCGAAGGUUACAAAAAGA	181	3243	GGCGAAGGUUACAAAAAGA	181	3265	UCUUUUUGUAACCUUCGCC	492
3261	AAGUACACAGCAGGUGAUG	182	3261	AAGUACACAGCAGGUGAUG	182	3283	CAUCACCUUCGUGUACUU	493
3279	GAGGAGUUUCUGAGGAGUG	183	3279	GAGGAGUUUCUGAGGAGUG	183	3301	CACUCCUCAGAAACUCCUC	494
3297	GACCACCCAGCCAUCCUUC	184	3297	GACCACCCAGCCAUCCUUC	184	3319	GAAGGAUGGUGGUGGUC	495
3315	CGGUCCCAGGCCCCGCUUGC	185	3315	CGGUCCCAGGCCCCGCUUGC	185	3337	GCAAGCGGGCCUGGGACCG	496
3333	CCUGGGUCCAUUGGCCUCC	186	3333	CCUGGGUCCAUUGGCCUCC	186	3355	GGAGGCCAUUGAACCCAGG	497
3351	CGAUCUCCCCUGGACACCA	187	3351	CGAUCUCCCCUGGACACCA	187	3373	UGGUGUCCAGGGGAGAUCCG	498
3369	AGCUCGCUCCUUAUACUG	188	3369	AGCUCGCUCCUUAUACUG	188	3391	CAGUAAGAGGACGGAGCU	499
3387	GCCGUGCAGCCCCAUAUGAG	189	3387	GCCGUGCAGCCCCAUAUGAG	189	3409	CCUCAUUGGGCUGCACGGC	500
3405	GGUGACAACGACUAUAUCA	190	3405	GGUGACAACGACUAUAUCA	190	3427	UGAUUAUGUGUUGUACAC	501
3423	AUCCCCUGCCUGACCCCA	191	3423	AUCCCCUGCCUGACCCCA	191	3445	UGGGGUCAGGCAGGGGGAU	502
3441	AAACCCGAGGUUGCUGACG	192	3441	AAACCCGAGGUUGCUGACG	192	3463	CGUCAGCAACCUCCGGUUU	503
3459	GAGGGCCACUUGGAGGGUU	193	3459	GAGGGCCACUUGGAGGGUU	193	3481	AACCCUCCAGUGGGCCUC	504
3477	UCCCCAGCCUAGCCAGCU	194	3477	UCCCCAGCCUAGCCAGCU	194	3499	AGCUGGCUAGGCGGGGGA	505
3495	UCCACCCUGAAUGAAGUCA	195	3495	UCCACCCUGAAUGAAGUCA	195	3517	UGACUUAUUCAGGGGUGGA	506
3513	AACACCUCCUACACCAUCU	196	3513	AACACCUCCUACACCAUCU	196	3535	AGAUGGUUAGGAGGUGUU	507
3531	UCCUGUGACAGCCCCCUGG	197	3531	UCCUGUGACAGCCCCCUGG	197	3553	CCAGGGGCGUCUCACAGGA	508
3549	GAGCCCCAGGACGAACCCAG	198	3549	GAGCCCCAGGACGAACCCAG	198	3571	CUUGUUCGUCUCCUGGGGUC	509
3567	GAGCCAGAGCCCCAGCUUG	199	3567	GAGCCAGAGCCCCAGCUUG	199	3589	CAAGCUUGGGGCUUGGGCUC	510
3585	GAGCUCCAGGUGGAGCCCG	200	3585	GAGCUCCAGGUGGAGCCCG	200	3607	CCGGCUCACCUCUGGAGCUC	511
3603	GAGCCAGAGCUGGAACAGU	201	3603	GAGCCAGAGCUGGAACAGU	201	3625	ACUGUUCAGCUCUGGCUC	512
3621	UUGCCGGAUUCGGGGUGCC	202	3621	UUGCCGGAUUCGGGGUGCC	202	3643	GGACCCCGAAUCCGGCAA	513
3639	CCUGCGCCUCCGGGCGGAAG	203	3639	CCUGCGCCUCCGGGCGGAAG	203	3661	CUUCGCGCCGAGGCGCAGG	514
3657	GCAGAGGAUAGCUUCCUGU	204	3657	GCAGAGGAUAGCUUCCUGU	204	3679	ACAGGAAGCUAUCCUCUGC	515
3675	UAGGGGCGUGGCCCCUACC	205	3675	UAGGGGCGUGGCCCCUACC	205	3697	GGUAGGGGCCAGCCCCCUA	516
3693	CCUGCCCCUGCCUGAAGCUC	206	3693	CCUGCCCCUGCCUGAAGCUC	206	3715	GAGCUUACAGGCAGGGCAGG	517
3711	CCCCCCCCUGCCAGCACCCA	207	3711	CCCCCCCCUGCCAGCACCCA	207	3733	UGGGUGCUGGCAGGGGGGG	518
3729	AGCAUCUCCUGGCCUGGCC	208	3729	AGCAUCUCCUGGCCUGGCC	208	3751	GGCCAGGCCAGGAGAUCCU	519
3747	CUGACCGGGCUUCCUGUCA	209	3747	CUGACCGGGCUUCCUGUCA	209	3769	UGACAGGAAGCCCCGGUCAG	520
3765	AGCCAGGCGUCCCCUUAUCA	210	3765	AGCCAGGCGUCCCCUUAUCA	210	3787	UGAUAAAGGCGACCUUGGCU	521
3783	AGCUGUCCCCUUCUGGAAG	211	3783	AGCUGUCCCCUUCUGGAAG	211	3805	CUUCCAGAAAGGGACAGCU	522
3801	GCUUUCUGCUCCUGACGUG	212	3801	GCUUUCUGCUCCUGACGUG	212	3823	CACGUCAGGAGCAGAAAGC	523
3819	GUUGUGCCCCAAACCCUUG	213	3819	GUUGUGCCCCAAACCCUUG	213	3841	CCAGGGUUUGGGGCACAAC	524
3837	GGGCGGCUUAGGAGGCAA	214	3837	GGGCGGCUUAGGAGGCAA	214	3859	UUGCCUCCUAAAGCCAGCCC	525
3855	AGAAAACUGCAGGGGCCCGU	215	3855	AGAAAACUGCAGGGGCCCGU	215	3877	ACGGCCCCUCGAGUUUUUCU	526
3873	UGACCAGCCCCUCUGCCUCC	216	3873	UGACCAGCCCCUCUGCCUCC	216	3895	GGAGGCGAGAGGGCUGGUGA	527

3891	CAGGAGGCCAACUGACUC	217	3891	CAGGAGGCCAACUGACUC	217	3913	GAGUCAGUUGGCCUCCUCG	528
3909	CUGAGCCAGGGUUCGCCCA	218	3909	CUGAGCCAGGGUUCGCCCA	218	3931	UGGGGAACCCUGGCUCAG	529
3927	AGGGAACUCAGUUUCCCA	219	3927	AGGGAACUCAGUUUCCCA	219	3949	UGGGAACUCAGUUUCCCU	530
3945	AUAUGUAAGAUGGGAAGU	220	3945	AUAUGUAAGAUGGGAAGU	220	3967	ACUUCCCAUCUUAACAUU	531
3963	UUAGGCUUGAUGACCCAGA	221	3963	UUAGGCUUGAUGACCCAGA	221	3985	UCUGGGUCAUCAAGCCUAA	532
3981	AAUCUAGGAUUCUCUCCCU	222	3981	AAUCUAGGAUUCUCUCCCU	222	4003	AGGGAGAGAAUCCUAGAUU	533
3999	UGGCUAGACAGGUGGGGAGA	223	3999	UGGCUAGACAGGUGGGGAGA	223	4021	UCUCCCCACCUUGUCAGCCA	534
4017	ACCGAAUCCUCCUUGGGA	224	4017	ACCGAAUCCUCCUUGGGA	224	4039	UCCAGGGAGGGGAUUCGGU	535
4035	AAGAUUCUUGGAGUUAUCUG	225	4035	AAGAUUCUUGGAGUUAUCUG	225	4057	CAGUAAUCUCCAAGAAUCUU	536
4053	GAGGUGGUAAAUUAACUUU	226	4053	GAGGUGGUAAAUUAACUUU	226	4075	AAAGUUAUUUACCAACUC	537
4071	UUUUCUGUUCAGCCAGCUA	227	4071	UUUUCUGUUCAGCCAGCUA	227	4093	UAGCUGGCUUGAACAGAAA	538
4089	ACCCUCUACAAGGAUUAUAG	228	4089	ACCCUCUACAAGGAUUAUAG	228	4111	CUAUGAUUCCUUGAGGGU	539
4107	GCUCUCUCCUCCGACUUAU	229	4107	GCUCUCUCCUCCGACUUAU	229	4129	AAAAGUGCGAGGAGAGC	540
4125	UUAUCCACCCAGGAGCUAG	230	4125	UUAUCCACCCAGGAGCUAG	230	4147	CUAGCUCUCCUGGGUGGAUA	541
4143	GGGAAGAGACCCUAGCCUC	231	4143	GGGAAGAGACCCUAGCCUC	231	4165	GAGGCUAGGGUCUCUCC	542
4161	CCUUGGCUUGGCUAGC	232	4161	CCUUGGCUUGGCUAGC	232	4183	GCUCAGCCAGCAGCCAGGG	543
4179	CUAGGGCCUAGCCUUGAGC	233	4179	CUAGGGCCUAGCCUUGAGC	233	4201	GCUCAGGCUAGGGCCUAG	544
4197	CAGUGUUGCCUUAUCCAGA	234	4197	CAGUGUUGCCUUAUCCAGA	234	4219	UCUGGAUGAGGCAACACUG	545
4215	AAGAAAGCCAGUCUCCUCC	235	4215	AAGAAAGCCAGUCUCCUCC	235	4237	GGAGGAGACUGGCUUUCUU	546
4233	CCUAGAUGCCAGUCCUCCUG	236	4233	CCUAGAUGCCAGUCCUCCUG	236	4255	CAGGACUGGCAUCAUAGG	547
4251	GCUGUCCUUGGCCCGAGCU	237	4251	GCUGUCCUUGGCCCGAGCU	237	4273	AGCUCGGCCAGGGAACGC	548
4269	UGGUCUGGGGCCAUUAAGGC	238	4269	UGGUCUGGGGCCAUUAAGGC	238	4291	GCCUAAUUGGCCCCAGACCA	549
4287	CAGCCUAAUUAUUGCUGGA	239	4287	CAGCCUAAUUAUUGCUGGA	239	4309	UCCAGCAUUAUUAAGGCG	550
4305	AGGCUAGGCCAAGUACAGG	240	4305	AGGCUAGGCCAAGUACAGG	240	4327	CCUGUACUUGGCUCAGCCU	551
4323	GACACCCCGAGCCUUGCAGC	241	4323	GACACCCCGAGCCUUGCAGC	241	4345	GCUGCAGGCUUGGGGUGUC	552
4341	CCCUUGCCCGAGGCGACUUG	242	4341	CCCUUGCCCGAGGCGACUUG	242	4363	CAAGUGCCUUGGGCAAGGG	553
4359	GGAGCACACGCGAGCCAUAG	243	4359	GGAGCACACGCGAGCCAUAG	243	4381	CUAUGGCUUGGUGGCUCC	554
4377	GCAAGUGCCUUGUCCUCCUG	244	4377	GCAAGUGCCUUGUCCUCCUG	244	4399	CAGGGACACAGGCGACUUGC	555
4395	GUCCUUCAGGCCCAUACAGU	245	4395	GUCCUUCAGGCCCAUACAGU	245	4417	ACUGAUGGGCCUGAAGGAC	556
4413	UCCUGGGGCUUUUUCUUUA	246	4413	UCCUGGGGCUUUUUCUUUA	246	4435	UAAAGAAAAAGCCCAAGGA	557
4431	AUCACCCUUCAGUCUUAUUC	247	4431	AUCACCCUUCAGUCUUAUUC	247	4453	GAUUAAGACUGAGGGUGAU	558
4449	CCAUCACCCAGAGUCUAGA	248	4449	CCAUCACCCAGAGUCUAGA	248	4471	UCUAGACUCUGGUGGAGG	559
4467	AAGGCCAGACGGGCCCGCG	249	4467	AAGGCCAGACGGGCCCGCG	249	4489	GCGGGGCCCGUCUGGCCUU	560
4485	CAUCUGUGAUGAGAAUGUA	250	4485	CAUCUGUGAUGAGAAUGUA	250	4507	UACAUUCUCAUCACAGAU	561
4503	AAUUGGCCAGUGUGGAGU	251	4503	AAUUGGCCAGUGUGGAGU	251	4525	ACUCCACACUGGCACAUUU	562
4521	UGGCCACGUGUGUGGCCA	252	4521	UGGCCACGUGUGUGGCCA	252	4543	UGGCACACACGUGGCCA	563
4539	AGUAUAGGCCCUUGGCUCU	253	4539	AGUAUAGGCCCUUGGCUCU	253	4561	AGAGCCAGGGCCCAUUAUCU	564

4557	UGCAUUGGACCUUGCUAUGA	254	4557	UGCAUUGGACCUUGCUAUGA	254	4579	UCAUAGCAGGUCCAAGCA	565
4575	AGGCUUUGGAGGAAUCCCU	255	4575	AGGCUUUGGAGGAAUCCCU	255	4597	AGGGAUCCUCCAAAGCCU	566
4593	UCACCCUCUCUGGGCCUCA	256	4593	UCACCCUCUCUGGGCCUCA	256	4615	UGAGGCCAGAGAGGGUGA	567
4611	AGUUCUCCCUUCAAACAAU	257	4611	AGUUCUCCCUUCAAACAAU	257	4633	AUUUUUUGAAGGGGAAACU	568
4629	UGAAUAGUCGGACUUAUU	258	4629	UGAAUAGUCGGACUUAUU	258	4651	AAUAAGUCCGACUUAUUA	569
4647	UAACUCUGAGUCCUUGCC	259	4647	UAACUCUGAGUCCUUGCC	259	4669	GGCAAGGCACUCAGAGUUA	570
4665	CAGCACUAACAUUCUAGAG	260	4665	CAGCACUAACAUUCUAGAG	260	4687	CUCUAGAAUGUUGAGUGCUG	571
4683	GUUUCCAGGUGGUUGCAC	261	4683	GUUUCCAGGUGGUUGCAC	261	4705	GUGCAACACCUUGGAAUAC	572
4701	CAUUUGUCCAGAUAGACA	262	4701	CAUUUGUCCAGAUAGACA	262	4723	UGCUUACUCUGGACAAUUG	573
4719	AAGGCCAUUAUACCCUAAAC	263	4719	AAGGCCAUUAUACCCUAAAC	263	4741	GUUUAGGGUUAUUGGCCUJU	574
4737	CUUCCAUCUUGGGGUCAG	264	4737	CUUCCAUCUUGGGGUCAG	264	4759	CUGACCCCGAGGAUGGAAG	575
4755	GCUGGGCUCCUGGGAGAUU	265	4755	GCUGGGCUCCUGGGAGAUU	265	4777	AAUCUCCAGGAGCCAGC	576
4773	UCCAGAUACACAUACACAC	266	4773	UCCAGAUACACAUACACAC	266	4795	GUGUGAUGUGUAUCUGGA	577
4791	CUCUGGGACUCAGGAACC	267	4791	CUCUGGGACUCAGGAACC	267	4813	GGUCCUGAGUCCCCAGAG	578
4809	CAUGCCCUUCCCGAGGCC	268	4809	CAUGCCCUUCCCGAGGCC	268	4831	GGCCUGGGGAAGGGGCAUG	579
4827	CCCCAGCAAGUUCAGAA	269	4827	CCCCAGCAAGUUCAGAA	269	4849	UUCUUGAGACUUGCUGGGG	580
4845	ACACAGCUGCACAGGCCUJ	270	4845	ACACAGCUGCACAGGCCUJ	270	4867	AAGCCUGUGCAGCUGUGU	581
4863	UGACUUAAGUAGACAGCCG	271	4863	UGACUUAAGUAGACAGCCG	271	4885	CGGCUGUCACUCUAAAGUCA	582
4881	GGUUCUUGGAAAGCCCCA	272	4881	GGUUCUUGGAAAGCCCCA	272	4903	UGGGGCUUCCAGGACACC	583
4899	AAGAGCUGCCCCAGGGAC	273	4899	AAGAGCUGCCCCAGGGAC	273	4921	GUCCUGGGGAGCUGCUU	584
4917	CAUGGGAAGACCACGGGAC	274	4917	CAUGGGAAGACCACGGGAC	274	4939	GUCCUGGUGUCUCCCAUG	585
4935	CCUUCUACUACCCACGA	275	4935	CCUUCUACUACCCACGA	275	4957	UCGUGGUAGUGAAAGAGG	586
4953	AUGACCUCCGGGGUUAUC	276	4953	AUGACCUCCGGGGUUAUC	276	4975	GGAUACCCCGGAGGUCAU	587
4971	CUGGGCAAAAGGGACAAAG	277	4971	CUGGGCAAAAGGGACAAAG	277	4993	CUUUGUCCCUUUUGCCCAG	588
4989	GAGGGCAAUAGAUACACC	278	4989	GAGGGCAAUAGAUACACC	278	5011	GGUGAUCUACAUUUGCCCUC	589
5007	CUCCUGCAGCCCACCACUC	279	5007	CUCCUGCAGCCCACCACUC	279	5029	GAGUGGUGGGCUGCAGGAG	590
5025	CCAGCACCUUGUCCGAGGU	280	5025	CCAGCACCUUGUCCGAGGU	280	5047	ACCUCGGCACAGGUGCUGG	591
5043	UCUGCGUCGAAGACAGAAU	281	5043	UCUGCGUCGAAGACAGAAU	281	5065	AUUCUGUCUUCGACGCGAGA	592
5061	UGGACAGUGAGGACAGUUA	282	5061	UGGACAGUGAGGACAGUUA	282	5083	UAACUGUCCUACACUGUCCA	593
5079	AUGUCUUGUAAAGACAAG	283	5079	AUGUCUUGUAAAGACAAG	283	5101	CUUGUCUUUUAACAAGACAU	594
5097	GAAGCUUCAGAUUGUACCC	284	5097	GAAGCUUCAGAUUGUACCC	284	5119	GGGUACCAUCUGAAGCUUC	595
5115	CCAAGAGGAUGUGAGAGG	285	5115	CCAAGAGGAUGUGAGAGG	285	5137	CCUCUCACAUCCUUCUUGG	596
5133	GUGGCCGCUUGGAGUUUGC	286	5133	GUGGCCGCUUGGAGUUUGC	286	5155	GCAACUCUCCAAAGCGGCCAC	597
5151	CCCCUACCCACCAGCUGC	287	5151	CCCCUACCCACCAGCUGC	287	5173	GCAGCUGGUGGGUGAGGGG	598
5169	CCCCAUCCUUGAGGCAGCG	288	5169	CCCCAUCCUUGAGGCAGCG	288	5191	CGCUGCCUCAGGGGAUGGGG	599
5187	GCUCCAUUGGGGUAUGGUU	289	5187	GCUCCAUUGGGGUAUGGUU	289	5209	AACCAUACCCCAUGGAGC	600
5205	UUUGUCACUCCCCAGACCU	290	5205	UUUGUCACUCCCCAGACCU	290	5227	AGGUCUGGGCAGUGACAAA	601

5223	UAGCAGUGACAUCUCAUUG	291	5223	UAGCAGUGACAUCUCAUUG	291	5245	CAAUGAGAUGACACUGCUA	602
5241	GUCCCCAGCCAGUGGGCA	292	5241	GUCCCCAGCCAGUGGGCA	292	5263	UGCCACACUGGGCUGGGAC	603
5259	AUUGAGGUGCCAGGGGAG	293	5259	AUUGAGGUGCCAGGGGAG	293	5281	CUCCCCUGGCACCCUCCAAU	604
5277	GUCAGGGUUGUAGCCAAGA	294	5277	GUCAGGGUUGUAGCCAAGA	294	5299	UCUUGGCUACAACCCUGAC	605
5295	ACGCCCCGCACGGGGAGG	295	5295	ACGCCCCGCACGGGGAGG	295	5317	CCUCCCCGUGCGGGGGCGU	606
5313	GGUUGGGAAGGGGUGCAG	296	5313	GGUUGGGAAGGGGUGCAG	296	5335	CUGCACCCCUUCCCAACC	607
5331	GGAAGCUCACCCCUUCUG	297	5331	GGAAGCUCACCCCUUCUG	297	5353	CCAGAGGGGUUGAGCUUCC	608
5349	GGACCAACCCUGCAUUGC	298	5349	GGACCAACCCUGCAUUGC	298	5371	GCAUUGCAGGGUUGGUGCC	609
5367	CAGGUUGGCACCUUACUUC	299	5367	CAGGUUGGCACCUUACUUC	299	5389	GAAGUAAGGUGCCAAACCUUG	610
5385	CCUUGGGAUCCCCAGAGUU	300	5385	CCUUGGGAUCCCCAGAGUU	300	5407	AACUCUGGGGAUCCAGGG	611
5403	UGGUCCAAGGAGGGAGAGU	301	5403	UGGUCCAAGGAGGGAGAGU	301	5425	ACUCUCCCUCCUUGGACCA	612
5421	UGGCUUCUCAAUACGGUAC	302	5421	UGGCUUCUCAAUACGGUAC	302	5443	GUACCGUAUUGAGAACCCA	613
5439	CCAAAGAUUAUAAUACCUA	303	5439	CCAAAGAUUAUAAUACCUA	303	5461	UAGGUGAUUAUUCUUUGG	614
5457	AGGUUUACAAUUAUUUUUA	304	5457	AGGUUUACAAUUAUUUUUA	304	5479	UAAAAUUAUUUGUAAACCU	615
5475	AGGACUCACGUUAACUCAC	305	5475	AGGACUCACGUUAACUCAC	305	5497	GUGAGUUAACGUGAGUCCU	616
5493	CAUUUAUACAGCAGAAAUG	306	5493	CAUUUAUACAGCAGAAAUG	306	5515	CAUUUCUGCUGUUAUAAAUG	617
5511	GCUAUUUUGUAGCUGUUA	307	5511	GCUAUUUUGUAGCUGUUA	307	5533	UACACGCAUACAAAAUAGC	618
5529	AAGUUUUUCUAUCUGUGUA	308	5529	AAGUUUUUCUAUCUGUGUA	308	5551	UACACAGAUAGAAAAACUU	619
5547	ACUUUUUUUUAAGGGAAAG	309	5547	ACUUUUUUUUAAGGGAAAG	309	5569	CUUUCUUUAAAAAAAAGU	620
5565	GAUUUUAAUUAUAAACCUUG	310	5565	GAUUUUAAUUAUAAACCUUG	310	5587	CAGGUUUAAUUAUAAAACU	621
5578	AACCUUGGUCUUCUCACUC	311	5578	AACCUUGGUCUUCUCACUC	311	5600	GAGUGAGAGCACCAGGUU	622

The 3'-ends of the Upper sequence and the Lower sequence of the siNA construct can include an overhang sequence, for example about 1, 2, 3, or 4 nucleotides in length, preferably 2 nucleotides in length, wherein the overhanging sequence of the lower sequence is optionally complementary to a portion of the target sequence. The upper sequence is also referred to as the sense strand, whereas the lower sequence is also referred to as the antisense strand. The upper and lower sequences in the Table can further comprise a chemical modification having Formulae I-VII or any combination thereof.

Table III: PDGFr Synthetic Modified siRNA constructs

Target Pos	Target	Seq ID	Aliases	Sequence	Seq ID
206	UGCCUGUCCUUCUACUCAGCUGU	623	PDGFRB:208U21 siRNA sense	CCUGUCCUUCUACUCAGCUTT	627
2918	CUCGAAUUAACAUCCCAAAGGCA	624	PDGFRB:2920U21 siRNA sense	CGAAUUAACAUCCCAAAGGTT	628
4567	CUGCUAUGAGGCUUUGGAGGAAU	625	PDGFRB:4569U21 siRNA sense	GCUAUGAGGCUUUGGAGGATT	629
4983	GACAAAGAGGGCAAUAGAGAUCA	626	PDGFRB:4985U21 siRNA sense	CAAGAGGGCAAUAGAGAUTT	630
206	UGCCUGUCCUUCUACUCAGCUGU	623	PDGFRB:226L21 siRNA (208C) antisense	AGCUGAGUAGAAGGACAGGTT	631
2918	CUCGAAUUAACAUCCCAAAGGCA	624	PDGFRB:2938L21 siRNA (2920C) antisense	CCUUUGGAGAUUAUUUCGTT	632
4567	CUGCUAUGAGGCUUUGGAGGAAU	625	PDGFRB:4587L21 siRNA (4569C) antisense	UCCUCCAAAGCCUCAUAGCTT	633
4983	GACAAAGAGGGCAAUAGAGAUCA	626	PDGFRB:5003L21 siRNA (4985C) antisense	AUCUCAUUUGCCCCUCUUUGTT	634
206	UGCCUGUCCUUCUACUCAGCUGU	623	PDGFRB:208U21 siRNA stab04 sense	B ccuGuccuuuuAcucAGcuTT B	635
2918	CUCGAAUUAACAUCCCAAAGGCA	624	PDGFRB:2920U21 siRNA stab04 sense	B cGAAuuuAcAucuccAAAGGTT B	636
4567	CUGCUAUGAGGCUUUGGAGGAAU	625	PDGFRB:4569U21 siRNA stab04 sense	B GcuAuGAGGcuuuuGGAGGATT B	637
4983	GACAAAGAGGGCAAUAGAGAUCA	626	PDGFRB:4985U21 siRNA stab04 sense	B cAAAGAGGGcAAAUAGAGuTT B	638
206	UGCCUGUCCUUCUACUCAGCUGU	623	PDGFRB:226L21 siRNA (208C) stab05 antisense	AGcuGAGuAGAAGGAGAGGTTsT	639
2918	CUCGAAUUAACAUCCCAAAGGCA	624	PDGFRB:2938L21 siRNA (2920C) stab05 antisense	ccuuuGGAGAUGuAAuuuGTTsT	640
4567	CUGCUAUGAGGCUUUGGAGGAAU	625	PDGFRB:4587L21 siRNA (4569C) stab05 antisense	uccuccAAAAGccucAuAGcTsT	641
4983	GACAAAGAGGGCAAUAGAGAUCA	626	PDGFRB:5003L21 siRNA (4985C) stab05 antisense	AucucAuuuGccccuuuuGTTsT	642
206	UGCCUGUCCUUCUACUCAGCUGU	623	PDGFRB:208U21 siRNA stab07 sense	B ccuGuccuuuuAcucAGcuTT B	643

2918	CUCGAAUUAUACAUCCCAAAGGCA	624	PDGFRB:2920U21 siRNA stab07 sense	B cGAAluuAcAucuccAAAGGTT B	644
4567	CUGCUAUGAGGCUUUGGAGGAU	625	PDGFRB:4569U21 siRNA stab07 sense	B GcuAuGAGGGcuuuGGAGGATT B	645
4983	GACAAAGAGGGCAAUUGAGAUCA	626	PDGFRB:4985U21 siRNA stab07 sense	B cAAAAGAGGGGcAAAUAGAGAU TT B	646
206	UGCCUGUCCUUCUACUCAGCUGU	623	PDGFRB:226L21 siRNA (208C) stab11 antisense	AGcuGAGuAGAAAGGAcAGGTsT	647
2918	CUCGAAUUAUACAUCCCAAAGGCA	624	PDGFRB:2938L21 siRNA (2920C) stab11 antisense	ccuuuGGAGAUGuAAuucGTsT	648
4567	CUGCUAUGAGGCUUUGGAGGAU	625	PDGFRB:4587L21 siRNA (4569C) stab11 antisense	uccuccAAA GccucAuAGcTsT	649
4983	GACAAAGAGGGCAAUUGAGAUCA	626	PDGFRB:5003L21 siRNA (4985C) stab11 antisense	AucucAuuuGccccuuuGTsT	650

Uppercase = ribonucleotide

u,c = 2'-deoxy-2'-fluoro U, C

T = thymidine

B = inverted deoxy abasic

s = phosphorothioate linkage

A = deoxy Adenosine

G = deoxy Guanosine

Table IV

Non-limiting examples of Stabilization Chemistries for chemically modified siNA constructs

Chemistry	pyrimidine	Purine	cap	p=S	Strand
"Stab 1"	Ribo	Ribo	-	5 at 5'-end 1 at 3'-end	S/AS
"Stab 2"	Ribo	Ribo	-	All linkages	Usually AS
"Stab 3"	2'-fluoro	Ribo	-	4 at 5'-end 4 at 3'-end	Usually S
"Stab 4"	2'-fluoro	Ribo	5' and 3'- ends	-	Usually S
"Stab 5"	2'-fluoro	Ribo	-	1 at 3'-end	Usually AS
"Stab 6"	2'-O-Methyl	Ribo	5' and 3'- ends	-	Usually S
"Stab 7"	2'-fluoro	2'-deoxy	5' and 3'- ends	-	Usually S
"Stab 8"	2'-fluoro	2'-O-Methyl	-	1 at 3'-end	Usually AS
"Stab 9"	Ribo	Ribo	5' and 3'- ends	-	Usually S
"Stab 10"	Ribo	Ribo	-	1 at 3'-end	Usually AS
"Stab 11"	2'-fluoro	2'-deoxy	-	1 at 3'-end	Usually AS

CAP = any terminal cap, see for example **Figure 10**.

All Stab 1-11 chemistries can comprise 3'-terminal thymidine (TT) residues

All Stab 1-11 chemistries typically comprise 21 nucleotides, but can vary as described herein.

S = sense strand

AS = antisense strand

Table V

A. 2.5 μ mol Synthesis Cycle ABI 394 Instrument

Reagent	Equivalents	Amount	Wait Time* DNA	Wait Time* 2'-O-methyl	Wait Time*RNA
Phosphoramidites	6.5	163 μ L	45 sec	2.5 min	7.5 min
S-Ethyl Tetrazole	23.8	238 μ L	45 sec	2.5 min	7.5 min
Acetic Anhydride	100	233 μ L	5 sec	5 sec	5 sec
N-Methyl Imidazole	186	233 μ L	5 sec	5 sec	5 sec
TCA	176	2.3 mL	21 sec	21 sec	21 sec
Iodine	11.2	1.7 mL	45 sec	45 sec	45 sec
Beaucage	12.9	645 μ L	100 sec	300 sec	300 sec
Acetonitrile	NA	6.67 mL	NA	NA	NA

B. 0.2 μ mol Synthesis Cycle ABI 394 Instrument

Reagent	Equivalents	Amount	Wait Time* DNA	Wait Time* 2'-O-methyl	Wait Time*RNA
Phosphoramidites	15	31 μ L	45 sec	233 sec	465 sec
S-Ethyl Tetrazole	38.7	31 μ L	45 sec	233 min	465 sec
Acetic Anhydride	655	124 μ L	5 sec	5 sec	5 sec
N-Methyl Imidazole	1245	124 μ L	5 sec	5 sec	5 sec
TCA	700	732 μ L	10 sec	10 sec	10 sec
Iodine	20.6	244 μ L	15 sec	15 sec	15 sec
Beaucage	7.7	232 μ L	100 sec	300 sec	300 sec
Acetonitrile	NA	2.64 mL	NA	NA	NA

C. 0.2 μ mol Synthesis Cycle 96 well Instrument

Reagent	Equivalents:DNA/ 2'-O-methyl/Ribo	Amount: DNA/2'-O- methyl/Ribo	Wait Time* DNA	Wait Time* 2'-O- methyl	Wait Time* Ribo
Phosphoramidites	22/33/66	40/60/120 μ L	60 sec	180 sec	360sec
S-Ethyl Tetrazole	70/105/210	40/60/120 μ L	60 sec	180 min	360 sec
Acetic Anhydride	265/265/265	50/50/50 μ L	10 sec	10 sec	10 sec
N-Methyl Imidazole	502/502/502	50/50/50 μ L	10 sec	10 sec	10 sec
TCA	238/475/475	250/500/500 μ L	15 sec	15 sec	15 sec
Iodine	6.8/6.8/6.8	80/80/80 μ L	30 sec	30 sec	30 sec
Beaucage	34/51/51	80/120/120	100 sec	200 sec	200 sec
Acetonitrile	NA	1150/1150/1150 μ L	NA	NA	NA

- Wait time does not include contact time during delivery.
- Tandem synthesis utilizes double coupling of linker molecule

CLAIMS

What we claim is:

1. A short interfering nucleic acid (siNA) molecule that down-regulates expression of a PDGFr gene by RNA interference.
2. The siNA molecule of claim 1, wherein the PDGFr gene encodes sequence comprising Genbank Accession number NM_002609.2.
3. The siNA molecule of claim 1, wherein said siNA molecule comprises no ribonucleotides.
4. The siNA molecule of claim 1, wherein said siNA molecule comprises ribonucleotides.
5. The siNA molecule of claim 1, wherein said siNA molecule is double stranded.
6. The siNA molecule of claim 5, wherein said siNA molecule comprises an antisense strand comprising a nucleotide sequence that is complementary to a nucleotide sequence or a portion thereof encoding a PDGFr protein, and wherein said siNA further comprises a sense strand, wherein said sense strand comprises a nucleotide sequence of a PDGFr gene or a portion thereof.
7. The siNA molecule of claim 6, wherein said antisense strand and said sense strand each comprise about 19 to about 29 nucleotides, and wherein said antisense strand and said sense strand share at least about 19 complementary nucleotides.
8. The siNA molecule of claim 5, wherein said siNA molecule comprises an antisense region comprising a nucleotide sequence that is complementary to a nucleotide sequence or a portion thereof encoding a PDGFr protein, and wherein said siNA further comprises a sense region, wherein said sense region comprises a nucleotide sequence of a PDGFr gene or a portion thereof.
9. The siNA molecule of claim 8, wherein said antisense region and said sense region each comprise about 19 to about 29 nucleotides, and wherein said antisense region and said sense region share at least about 19 complementary nucleotides.
10. The siNA molecule of claim 1, wherein said siNA molecule is single stranded.

11. The siNA molecule of claim 10, wherein said siNA comprises a nucleotide sequence that is complementary to a nucleotide sequence or a portion thereof encoding a PDGFr protein.
12. The siNA molecule of claim 11, wherein said siNA molecule comprises a sequence having about 19 to about 29 nucleotides.
13. The siNA molecule of claim 1, wherein said siNA molecule comprises a sense region and an antisense region and wherein said antisense region comprises a nucleotide sequence that is complementary to a nucleotide sequence or a portion thereof encoding a PDGFr protein and said sense region comprises a nucleotide sequence complementary to said antisense region.
14. The siNA molecule of claim 1, wherein said siNA molecule is assembled from two oligonucleotide fragments wherein one fragment comprises a sense region and a second fragment comprises an antisense region of said siNA molecule.
15. The siNA molecule of claim 13, wherein said sense region and said antisense region comprise separate oligonucleotides.
16. The siNA molecule of claim 13, wherein said sense region and said antisense region are connected via a linker molecule.
17. The siNA molecule of claim 16, wherein said linker molecule is a polynucleotide linker.
18. The siNA molecule of claim 16, wherein said linker molecule is a non-nucleotide linker.
19. The siNA molecule of claim 13, wherein said sense region comprises a 3'-terminal overhang and said antisense region comprises a 3'-terminal overhang.
20. The siNA molecule of claim 19, wherein said 3'-terminal overhangs each comprise about 2 nucleotides.
21. The siNA molecule of claim 19, wherein the 3'-terminal overhang of the antisense region is complementary to RNA encoding a PDGFr protein.
22. The siNA molecule of claim 13, wherein said sense region comprises one or more 2'-O-methyl pyrimidine nucleotides and one or more 2'-deoxy purine nucleotides.

23. The siNA molecule of claim 13, wherein any pyrimidine nucleotides present in said sense region comprise 2'-deoxy-2'-fluoro pyrimidine nucleotides and wherein any purine nucleotides present in said sense region comprise 2'-deoxy purine nucleotides.
24. The siNA molecule of claim 19, wherein any nucleotides comprising a 3'-terminal nucleotide overhang that are present in said sense region are 2'-deoxy nucleotides.
25. The siNA molecule of claim 13, wherein said sense region comprises a 3'-end and a 5'-end, and wherein a terminal cap moiety is present at the 5'-end, the 3'-end, or both of the 5' and 3' ends of said sense region.
26. The siNA molecule of claim 25, wherein said terminal cap moiety is an inverted deoxy abasic moiety.
27. The siNA molecule of claim 13, wherein said antisense region comprises one or more 2'-deoxy-2'-fluoro pyrimidine nucleotides and one or more 2'-O-methyl purine nucleotides.
28. The siNA molecule of claim 13, wherein any pyrimidine nucleotides present in said antisense region comprise 2'-deoxy-2'-fluoro pyrimidine nucleotides and wherein any purine nucleotides present in said antisense region comprise 2'-O-methyl purine nucleotides.
29. The siNA molecule of claim 19, wherein any nucleotides comprising a 3'-terminal nucleotide overhang that are present in said antisense region are 2'-deoxy nucleotides.
30. The siNA molecule of claim 28, wherein said antisense region comprises a phosphorothioate internucleotide linkage at the 3' end of said antisense region.
31. The siNA molecule of claim 13, wherein said antisense region comprises a glyceryl modification at the 3' end of said antisense region.
32. The siNA molecule of claim 19, wherein said 3'-terminal overhangs comprise deoxyribonucleotides.

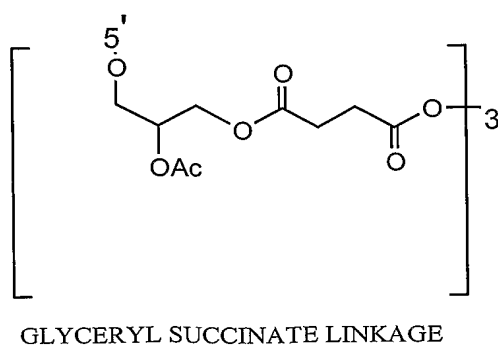
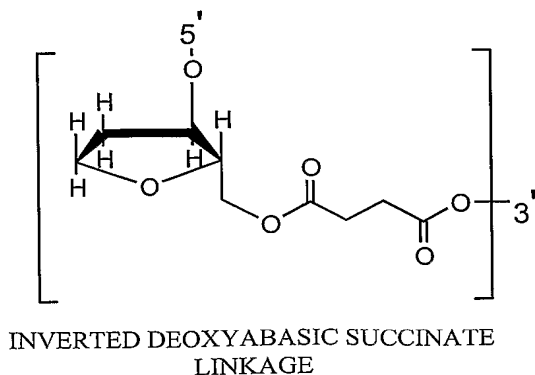
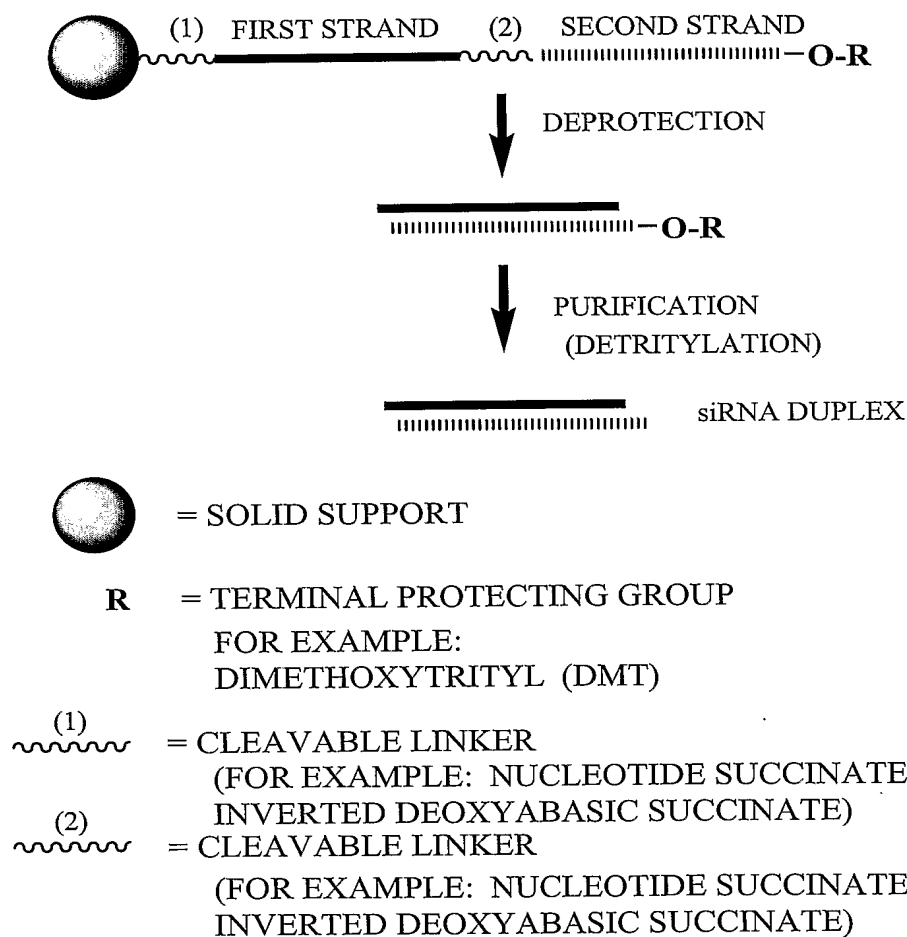
Figure 1

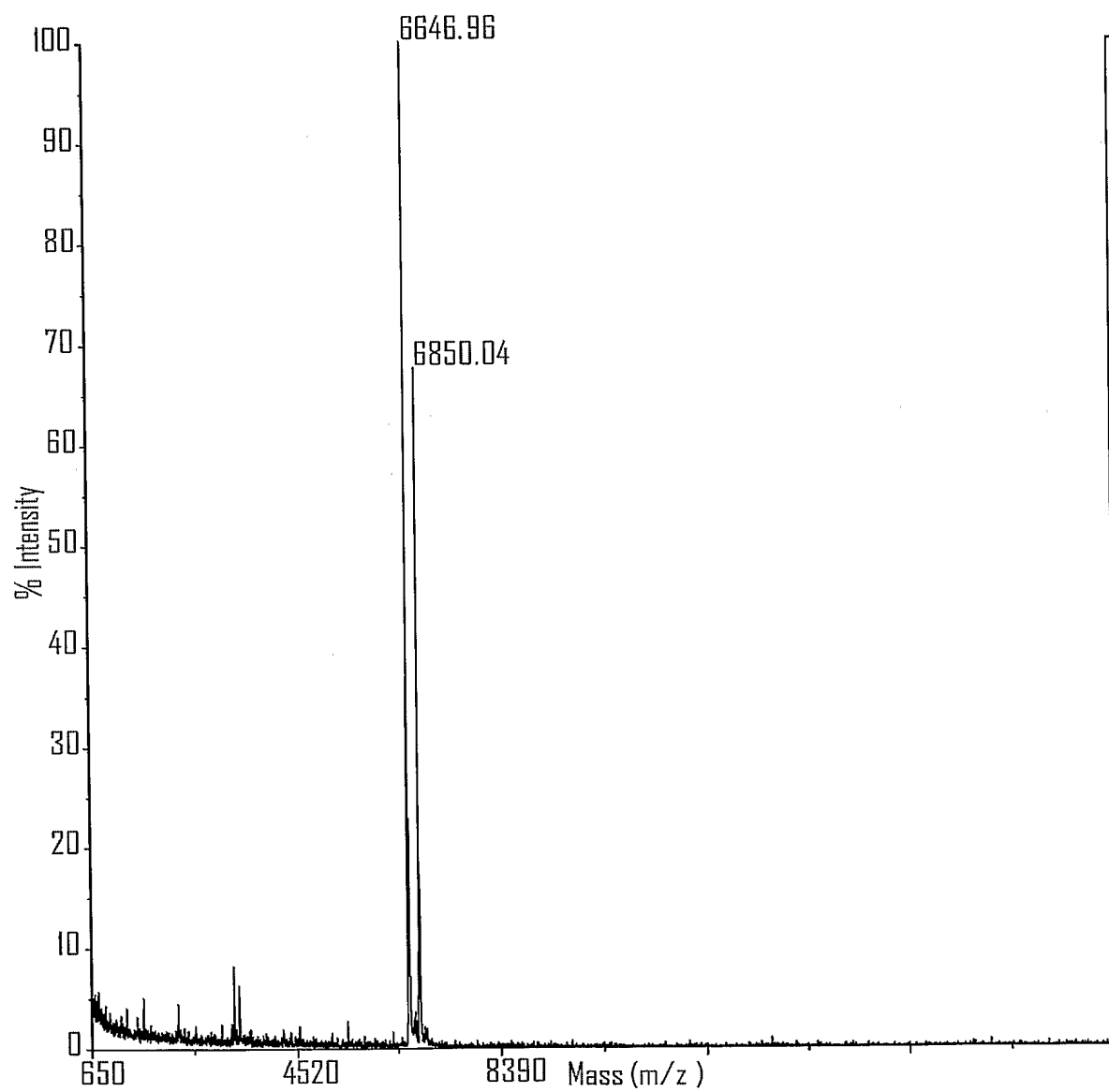
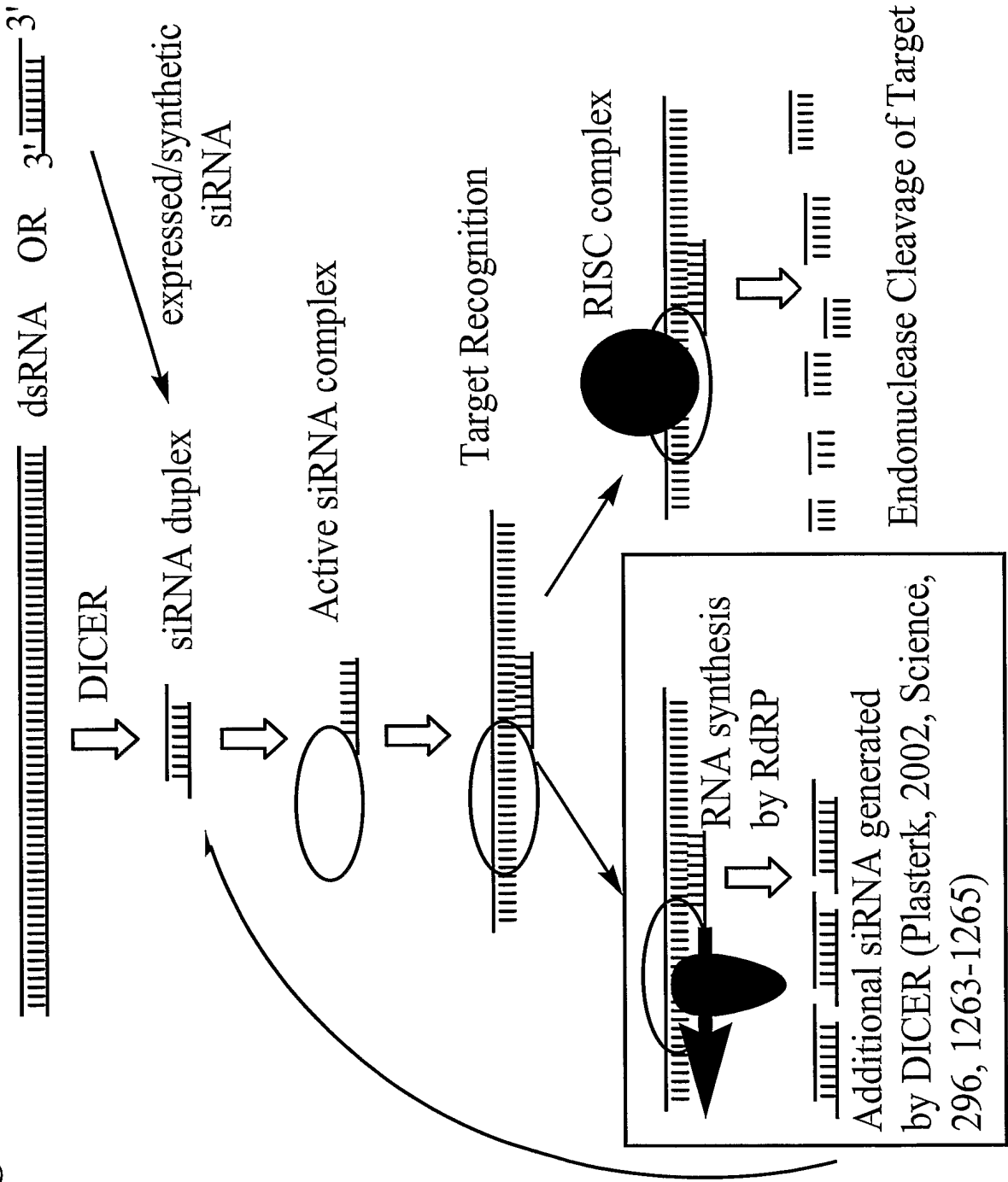
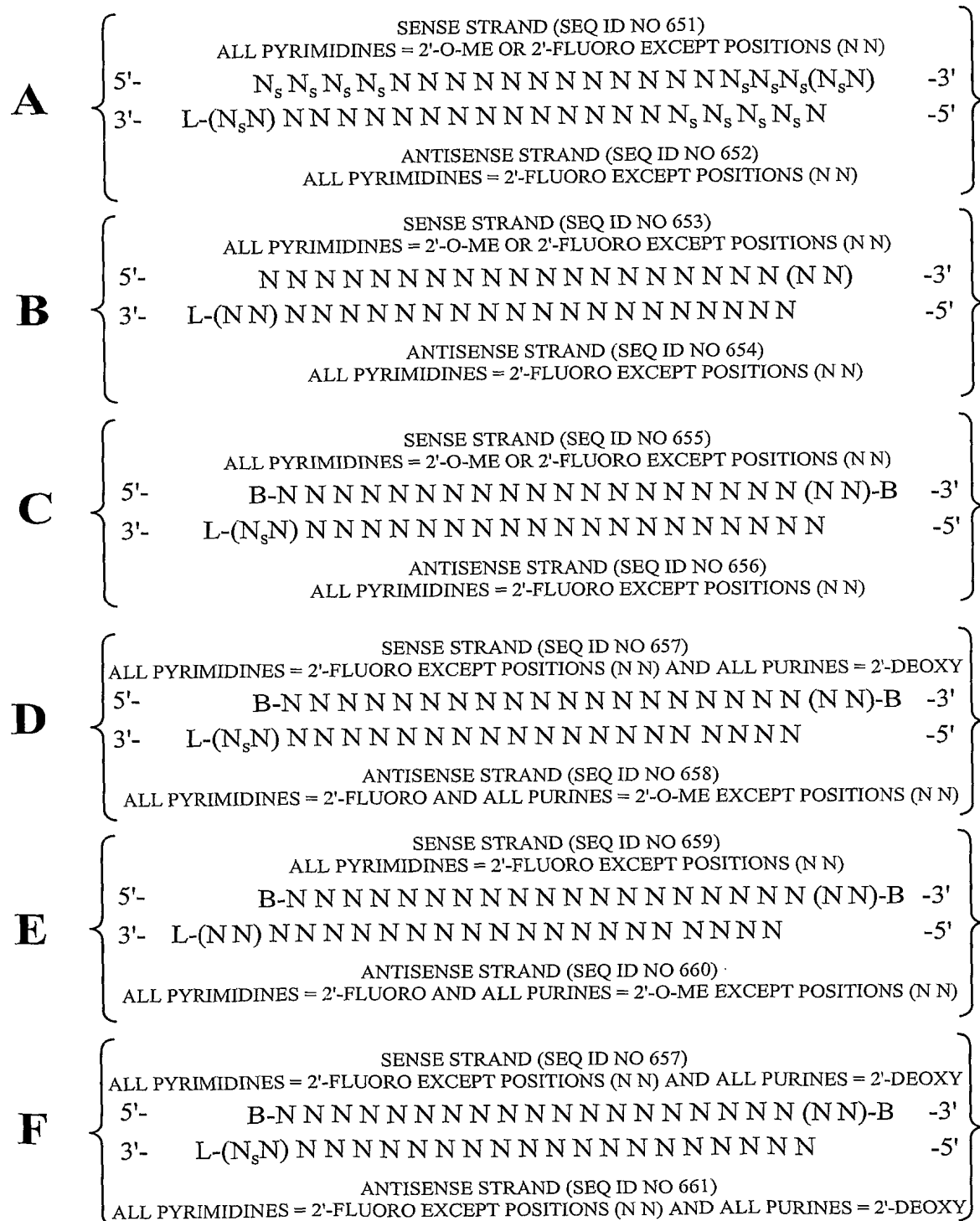
Figure 2

Figure 3



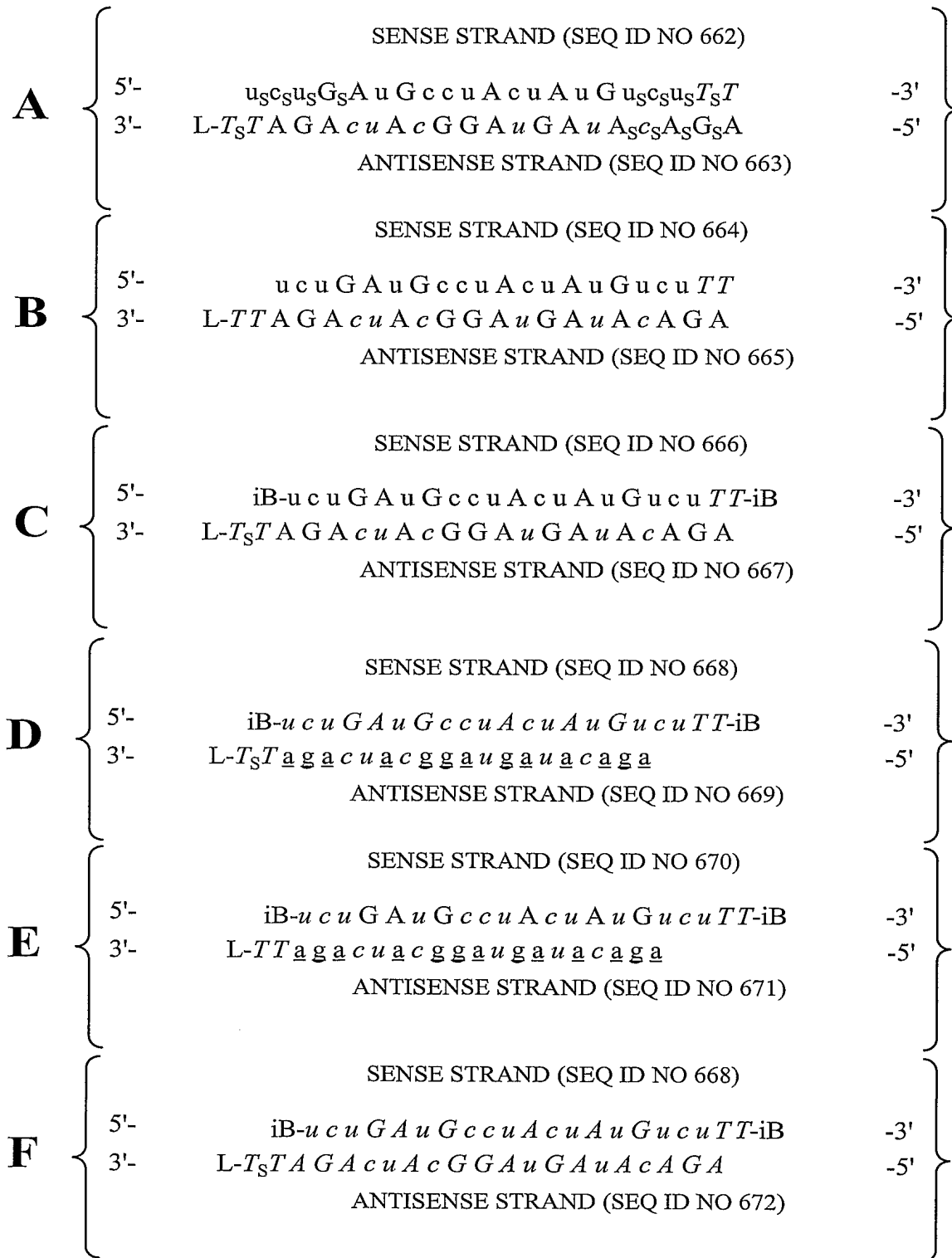


POSITIONS (NN) CAN COMPRISE ANY NUCLEOTIDE, SUCH AS DEOXYNUCLEOTIDES (eg. THYMIDINE) OR UNIVERSAL BASES

B = ABASIC, INVERTED ABASIC, INVERTED NUCLEOTIDE OR OTHER TERMINAL CAP THAT IS OPTIONALLY PRESENT

L = GLYCERYL MOIETY THAT IS OPTIONALLY PRESENT

S = PHOSPHOROTHIOATE OR PHOSPHORODITHIOATE



lower case = 2'-O-Methyl or 2'-deoxy-2'-fluoro

italic lower case = 2'-deoxy-2'-fluorounderline = 2'-O-methyl*ITALIC UPPER CASE* = DEOXY

B = INVERTED DEOXYABASIC

L = GLYCERYL MOIETY OPTIONALLY PRESENT

S = PHOSPHOROTHIOATE OR

PHOSPHORODITHIOATE

Figure 6

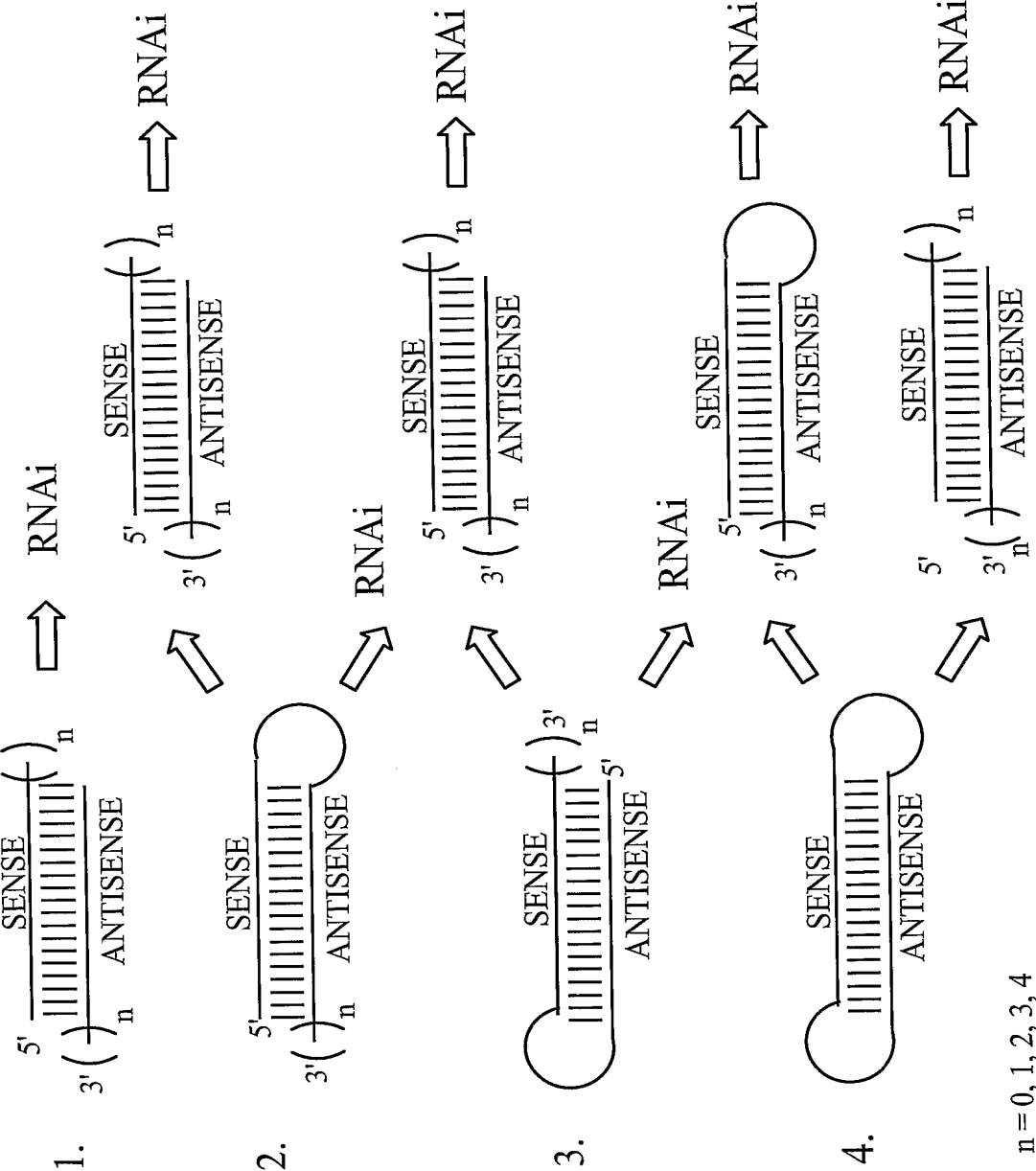


Figure 9: Target site Selection using siRNA

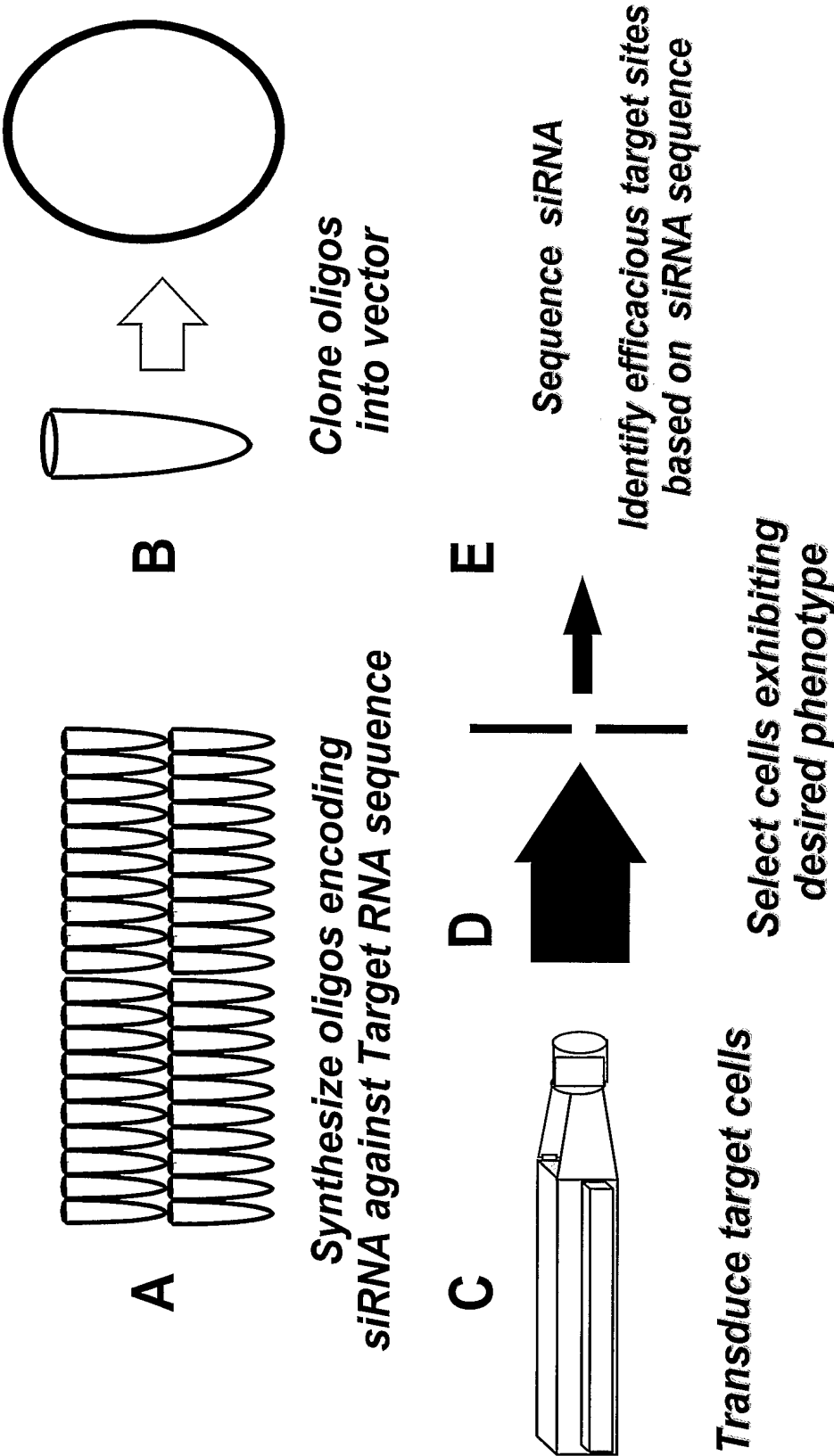
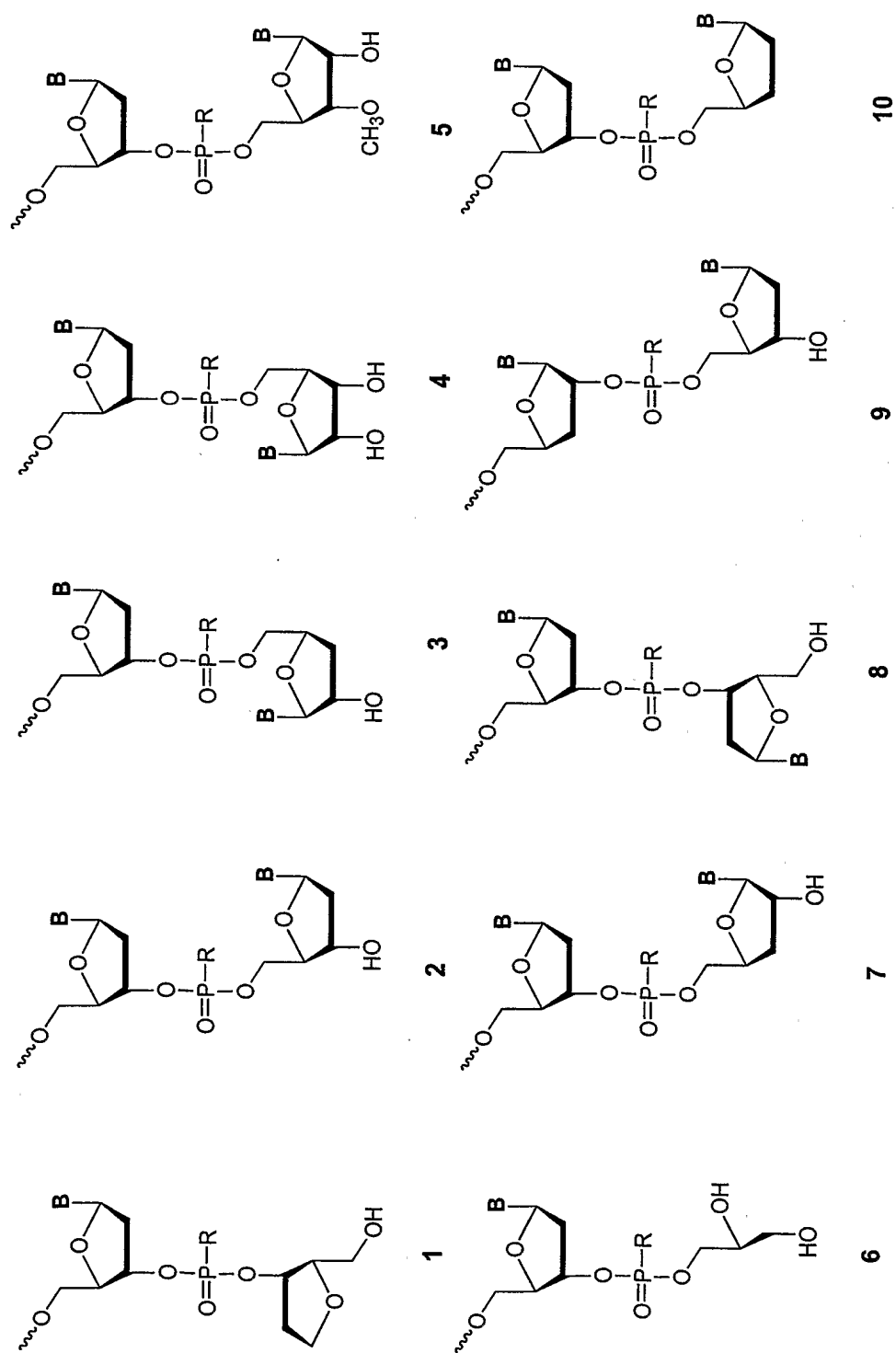


Figure 10

R = O, S, N, alkyl, substituted alkyl, O-alkyl, S-alkyl, alkaryl, or aralkyl
 B = Independently any nucleotide base, either naturally occurring or chemically modified, or optionally H (abasic).

Figure 11: Modification Strategy

